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## OM protein - protein search, using sw model

Run on: June 7, 2003, 12:06:35 ; Search time 14 Seconds

(Without alignments)  
323.652 Million cell updates/sec

Title: US-09-579-548a-1\_COPY\_108\_261

Sequence score: 792 1 ENSFEMQKDONPOIAAHVI.....TDPQVSHGTGFTSFGILKL 154

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 212163

Minimum DB seq length: 0

Maximum DB seq length: 154

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfilltest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	96.7	149	3	US-08-584-031-16
2	755	95.3	151	1	US-07-940-605A-3
3	755	95.3	151	2	US-08-690-096-3
4	751	94.8	146	4	US-08-637-323-1
5	567	71.6	151	1	US-07-940-605A-4
6	567	71.6	151	2	US-08-690-096-4
7	128	16.2	154	1	US-07-994-469A-75
8	122.5	15.5	150	1	US-07-994-469A-57
9	121	15.3	139	1	US-07-994-469A-10
10	121	15.3	145	1	US-07-994-469A-9
11	121	15.3	150	1	US-07-668-517-14
12	121	15.3	150	1	US-07-668-517-35
13	121	15.3	150	1	US-07-668-517-36
14	121	15.3	150	4	US-09-286-529-25
15	121	15.3	151	1	US-07-668-517-7
16	121	15.3	151	1	US-07-668-517-28
17	121	15.3	152	1	US-07-668-517-36
18	121	15.3	152	1	US-07-668-517-21
19	119.5	15.1	147	4	US-09-105-343A-9
20	119	15.0	150	1	US-07-668-517-8
21	119	15.0	150	1	US-07-668-517-9
22	119	15.0	150	1	US-07-668-517-12
23	119	15.0	150	1	US-07-668-517-13
24	119	15.0	150	1	US-07-994-469A-7
25	119	15.0	150	1	US-07-994-469A-8
26	119	15.0	151	1	US-07-668-517-22
27	119	15.0	151	1	US-07-668-517-23

28	119	15.0	151	1	US-07-668-517-26	Sequence 26, Appl
29	119	15.0	151	1	US-07-668-517-27	Sequence 27, Appl
30	118	14.9	147	1	US-07-668-517-1	Sequence 1, Appl
31	118	14.9	148	1	US-07-668-517-2	Sequence 2, Appl
32	118	14.9	148	1	US-07-668-517-15	Sequence 15, Appl
33	118	14.9	149	1	US-07-668-517-3	Sequence 3, Appl
34	118	14.9	149	1	US-07-668-517-16	Sequence 16, Appl
35	118	14.9	150	1	US-07-668-517-4	Sequence 4, Appl
36	118	14.9	150	1	US-07-668-517-5	Sequence 5, Appl
37	118	14.9	150	1	US-07-668-517-6	Sequence 6, Appl
38	118	14.9	150	1	US-07-668-517-10	Sequence 10, Appl
39	118	14.9	150	1	US-07-668-517-11	Sequence 11, Appl
40	118	14.9	150	1	US-07-668-517-17	Sequence 17, Appl
41	118	14.9	151	1	US-07-668-517-37	Sequence 37, Appl
42	118	14.9	151	1	US-07-668-517-18	Sequence 18, Appl
43	118	14.9	151	1	US-07-668-517-19	Sequence 19, Appl
44	118	14.9	151	1	US-07-668-517-20	Sequence 20, Appl
45	118	14.9	151	1	US-07-668-517-24	Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-08-584-031-16  
Sequence 16, Application US/08584031A  
Patent No. 6030945  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: APO-2 LIGAND  
FILE REFERENCE: 11669.220S03  
CURRENT APPLICATION NUMBER: US/08/584,031A  
CURRENT FILING DATE: 1996-01-09  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-584-031-16

Query Match 96.7%; Score 766; DB 3; Length 149;  
Best Local Similarity 100.0%; Pred. No. 2.4e-86;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	6	MOKGDONPOIAAHVISEASSKTSVLOMAEKGYTMSNNLVTLNKGKLTIVKQGLYYIY	65
DB	1	MOKGDONPOIAAHVISEASSKTSVLOMAEKGYTMSNNLVTLNKGKLTIVKQGLYYIY	60
QY	66	AQVTFCSNREASSQAPFIASLCUKSPGRPERILLRANTHSSAKPCGQOSIHIGVPELQ	125
DB	61	AQVTFCSNREASSQAPFIASLCUKSPGRPERILLRANTHSSAKPCGQOSIHIGVPELQ	120
QY	126	PGASVFVNVTDPQVSHGTGFTSFGILKL	154
DB	121	PGASVFVNVTDPQVSHGTGFTSFGILKL	149

RESULT 2  
US-07-940-605A-3  
Sequence 3, Application US/07940605A  
Patent No. 5540926  
GENERAL INFORMATION:  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: HOLLENBAUGH, DIANE  
APPLICANT: LEDBETTER, JEFFREY A.  
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York

COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/940,605A  
FILING DATE: 04-SEP-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-940-605A-3

Query Match 95.3%; Score 755; DB 1; Length 151;  
Best Local Similarity 98.7%; Pred. No. 5,5e-85;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FEMQKQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLNKGKLTVRQGLYY 63  
Db 1 FEMQKQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLNKGKLTVRQGLYY 60  
Qy 64 IYAQVTFCSNRSSQAPFLASLCLKSPGRERILLRANHTSSAKPGQOSIHLGVFE 123  
Db 61 IYAQVTFCSNRSSQAPFLASLCLKSPGRERILLRANHTSSAKPGQOSIHLGVFE 120  
Qy 124 LQPGASVFVNTDPSQVSHGTGFTSFGILKL 154  
Db 121 LQPGASVFVNTDPSQVSHGTGFTSFGILKL 151

RESULT 3  
US-08-690-096-3  
Sequence 3, Application US/08690096  
Patent No. 5945513  
GENERAL INFORMATION:  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: HOLLENAUGH, DIANE  
APPLICANT: LEDBETTER, JEFFREY A.  
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,096  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/940,605  
FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-690-096-3

Query Match 95.3%; Score 755; DB 2; Length 151;  
Best Local Similarity 98.7%; Pred. No. 5,5e-85;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FEMQKQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLNKGKLTVRQGLYY 63  
Db 1 FEMQKQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLNKGKLTVRQGLYY 60  
Qy 64 IYAQVTFCSNRSSQAPFLASLCLKSPGRERILLRANHTSSAKPGQOSIHLGVFE 123  
Db 61 IYAQVTFCSNRSSQAPFLASLCLKSPGRERILLRANHTSSAKPGQOSIHLGVFE 120  
Qy 124 LQPGASVFVNTDPSQVSHGTGFTSFGILKL 154  
Db 121 LQPGASVFVNTDPSQVSHGTGFTSFGILKL 151

RESULT 4  
US-08-637-323-1  
Sequence 1, Application US/08637323  
Patent No. 6340459  
GENERAL INFORMATION:  
APPLICANT: Yellin, Michael J.  
APPLICANT: Lederman, Seth  
APPLICANT: Chess, Leonard  
APPLICANT: Karpusas, Michael N.  
APPLICANT: Thomas, David W.  
TITLE OF INVENTION: THERAPEUTIC APPLICATIONS FOR THE ANTI-T-BAM (CD40-L)  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/637,323  
FILING DATE: Herewith  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/566,258  
FILING DATE: 01-DEC-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/567,391  
FILING DATE: 01-DEC-1995  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: White Bsq., John P.  
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 47279-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278 0400  
TELEFAX: (212)391 0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-08-637-323-1

Query Match 94.8%; Score 751; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 1,6e-84;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GQONPOIAAHVISEASSTTSVYLQMAEKGYTMSNNLVLTENGKQLTVRQGLYYIYAOV 68  
DB 1 GQONPOIAAHVISEASSTTSVYLQMAEKGYTMSNNLVLTENGKQLTVRQGLYYIYAOV 60  
QY 69 TFCNSREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPCGQOSIHLGCVFELQPCA 128  
DB 61 TFCNSREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPCGQOSIHLGCVFELQPCA 120  
QY 129 SVFVNVTPDSQVSHGTGFTSFGILKL 154  
DB 121 SVFVNVTPDSQVSHGTGFTSFGILKL 146

RESULT 5  
US-07-940-605A-4

Sequence 4, Application US/07940605A  
Patent No. 5540926

GENERAL INFORMATION:

APPLICANT: ARUPFO, ALEJANDRO

APPLICANT: HOLLENBAUGH, DIANE

APPLICANT: LEDBETTER, JEFFREY A.

TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/940,605A

FILING DATE: 04-SEP-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 869-8864/9741

TELEFAX: 212 869-8864/9741

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-940-605A-4

Query Match 71.6%; Score 567; DB 1; Length 151;

Best Local Similarity 73.5%; Pred. No. 7.1e-62;  
Matches 111; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

QY 4 FEMOKGQONPOIAAHVISEASSTTSVYLQMAEKGYTMSNNLVLTENGKQLTVRQGLYY 63  
DB 1 FEMOKGQONPOIAAHVISEASSTTSVYLQMAEKGYTMSNNLVLTENGKQLTVRQGLYY 60  
QY 64 IYAQVTFCSNREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPCGQOSIHLGCVFE 123  
DB 61 IYAQVTFCSNREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPCGQOSIHLGCVFE 120  
QY 124 LQAGASVFVNVTPDSQVSHGTGFTSFGILKL 154  
DB 121 LQAGASVFVNVTPDSQVSHGTGFTSFGILKL 151

RESULT 6

US-08-690-096-4

Sequence 4, Application US/0869096

Patent No. 5945513

GENERAL INFORMATION:

APPLICANT: ARUPFO, ALEJANDRO

APPLICANT: HOLLENBAUGH, DIANE

APPLICANT: LEDBETTER, JEFFREY A.

TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/690,096

FILING DATE: 31-JUL-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/940,605

FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 869-8864/9741

TELEFAX: 212 869-8864/9741

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-690-096-4

Query Match 71.6%; Score 567; DB 2; Length 151;

Best Local Similarity 73.5%; Pred. No. 7.1e-62;

Matches 111; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

QY 4 FEMOKGQONPOIAAHVISEASSTTSVYLQMAEKGYTMSNNLVLTENGKQLTVRQGLYY 63  
DB 1 FEMOKGQONPOIAAHVISEASSTTSVYLQMAEKGYTMSNNLVLTENGKQLTVRQGLYY 60  
QY 64 IYAQVTFCSNREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPCGQOSIHLGCVFE 123  
DB 61 IYAQVTFCSNREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPCGQOSIHLGCVFE 120



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COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,469A
; FILING DATE: 21-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5519119man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 72-085-0 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-994-469A-10

Query Match 15.3%; Score 121; DB 1; Length 139;
Best Local Similarity 29.3%; Pred. No. 4.1e-07;
Matches 41; Conservative 25; Mismatches 68; Indels 6; Gaps 5;

Cy 17 AHVISEASKTTSYLQNAEKGYTMSNNLVTLENGKQLTVKROGLYTYAQTFCSNREA 76
Db 4 AHVV--ANPQAEGLQMLNRRANALLANGVELRD-NQLVSESGILYISQVLFKGGCCP 60
Cy 77 SSQAPFIASLCLKSPREFRI-LIRAAHTSSAKPCGQOSIHLGVPFELQPGASVFNVT 135
Db 61 STHVLTTHTISRIAVSYQTKVNLISAKSPCEAKR-WPEPIYLGVPFLEKGRDLRAEIN 119
Cy 136 DPSOVSHG-TGFTSFGLIKL 154
Db 120 RPDYLDFAESGQVYFGIALL 139

RESULT 10
US-07-994-469A-9
; Sequence 9, Application US/07994469A
; Patent No. 5519119
; GENERAL INFORMATION:
; APPLICANT: Yamada, No. 5519119utosh
; APPLICANT: Kato, Masanari
; APPLICANT: Miyata, Keizo
; APPLICANT: Aoyama, Yoshiyuki
; APPLICANT: Shikama, Hiroshi
; TITLE OF INVENTION: Polypeptide
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,469A
; FILING DATE: 21-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5519119man F.
; REGISTRATION NUMBER: 24,618
```

```
REFERENCE/DOCKET NUMBER: 72-085-0 FWC
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-994-469A-9

Query Match 15.3%; Score 121; DB 1; Length 145;
Best Local Similarity 29.3%; Pred. No. 4.4e-07;
Matches 41; Conservative 25; Mismatches 68; Indels 6; Gaps 5;

Cy 17 AHVISEASKTTSYLQNAEKGYTMSNNLVTLENGKQLTVKROGLYTYAQTFCSNREA 76
Db 10 AHVV--ANPQAEGLQMLNRRANALLANGVELRD-NQLVSESGILYISQVLFKGGCCP 66
Cy 77 SSQAPFIASLCLKSPREFRI-LIRAAHTSSAKPCGQOSIHLGVPFELQPGASVFNVT 135
Db 67 STHVLTTHTISRIAVSYQTKVNLISAKSPCEAKR-WPEPIYLGVPFLEKGRDLRAEIN 125
Cy 136 DPSOVSHG-TGFTSFGLIKL 154
Db 126 RPDYLDFAESGQVYFGIALL 145

RESULT 11
US-07-668-517-14
; Sequence 14, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el. Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Displaywrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
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FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-668-517-14

Query Match 15.3%; Score 121; DB 1; Length 150;  
Best Local Similarity 28.6%; Pred. No. 4.6e-07;  
Matches 44; Conservative 21; Mismatches 63; Indels 26; Gaps 6;

QY 17 AHVISEASKTSVLOWAEKGYTMSNNLVTLNGKQITVKROGLYYIAQVTF----- 70  
DB 7 AHVV--ANPQAEQQLQMLNRRANALLANGVELRD-NQLVVPSEGLYIYSQVLFKGGCP 63  
QY 71 -----CSNREASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHLGCV 121  
DB 64 STHVLLHTHTISRIAVSYQTKVNLISAKSPQ-----RETPEGAEAKP-WPEPIYLGCV 116  
QY 122 FELQPGASVFVNTDPSQVSHG-TGFTSPGLKL 154  
DB 117 FOLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 150

## RESULT 12

US-07-668-517-35  
Sequence 35, Application US/07668517  
Patent No. 5262309

GENERAL INFORMATION:

APPLICANT: Satoshi NAKAMURA et al.

TITLE OF INVENTION: No. 5262309el Physiologically Active

TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 KB

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668,517

FILING DATE: 19910322

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-07-668-517-35

Query Match 15.3%; Score 121; DB 1; Length 150;  
Best Local Similarity 28.6%; Pred. No. 4.6e-07;  
Matches 44; Conservative 20; Mismatches 64; Indels 26; Gaps 6;

QY 17 AHVISEASKTSVLOWAEKGYTMSNNLVTLNGKQITVKROGLYYIAQVTF----- 70  
DB 7 AHVV--ANPQAEQQLQMLNRRANALLANGVELRN-NSLVVPSEGLYIYSQVLFKGGCP 63  
QY 71 -----CSNREASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHLGCV 121  
DB 64 STHVLLHTHTISRIAVSYQTKVNLISAKSPQ-----RETPEGAEAKP-WPEPIYLGCV 116  
QY 122 FELQPGASVFVNTDPSQVSHG-TGFTSPGLKL 154  
DB 117 FOLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 150

## RESULT 13

US-07-994-469A-6  
Sequence 6, Application US/07994469A  
Patent No. 5519119

GENERAL INFORMATION:

APPLICANT: Yamada, No. 5519119utoshi

APPLICANT: Kato, Masanari

APPLICANT: Miyata, Keizo

APPLICANT: Aoyama, Yoshiyuki

APPLICANT: Shikama, Hiroshi

TITLE OF INVENTION: Polypeptide

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/994,469A

FILING DATE: 21-DEC-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5519119man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 72-085-0 FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)413-3000

TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-994-469A-6

Query Match 15.3%; Score 121; DB 1; Length 150;  
Best Local Similarity 28.6%; Pred. No. 4.6e-07;  
Matches 44; Conservative 21; Mismatches 63; Indels 26; Gaps 6;

QY 17 AHVISEASKTSVLOWAEKGYTMSNNLVTLNGKQITVKROGLYYIAQVTF----- 70  
DB 7 AHVV--ANPQAEQQLQMLNRRANALLANGVELRD-NQLVVPSEGLYIYSQVLFKGGCP 63  
QY 71 -----CSNREASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHLGCV 121  
DB 64 STHVLLHTHTISRIAVSYQTKVNLISAKSPQ-----RETPEGAEAKP-WPEPIYLGCV 116

**OY** 122 FELDPCASVFVNVTDPSSQVSHG-TGFSTFGLLKL 154  
|::| : : | ::||::|  
**Dib** 117 FQLEKGDRLSAEINRPDIYDLPAESGGVYFGIIAL 150

### RESULT 14

```

US-09-286-529-25
/ Sequence 25, Application US/09286529
/ Patent No. 6297367
/
/ GENERAL INFORMATION:
/ APPLICANT: Catheline Tribouley
/ TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
/ FILE REFERENCE: 1408.003/200130.439c1
/ CURRENT APPLICATION NUMBER: US/09/286,529
/ CURRENT FILING DATE: 1999-04-05
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/
/ LENGTH: 150
/ TYPE: PRT
/
/ ORGANISM: Homo sapien
US-09-286-529-25

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Query Match	15.3%	Score 121;	DB 4;	Length 150;
Best Local Similarity	28.6%	Pred. No. 4.6e-07;		
Matches 44;	Conservative 21;	Mismatches 63;	Indels 26;	Gaps 6

[illegible]

### RESULT 15

US-07-668-517-7  
Sequence 7, Application US/07668517  
Patent No. 5262309  
GENERAL INFORMATION:  
APPLICANT: Satoshi NAKAMURA et al.  
TITLE OF INVENTION: No. 5262309el Physiologically Active  
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,517  
FILING DATE: 19910322  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154

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? REFERENCE/DOCKET NUMBER:
? TELECOMMUNICATION INFORMATION
? TELEPHONE: 202-371-8850
? TELEFAX: 202-371-8856
? TELEX:
?
? INFORMATION FOR SEQ ID NO: 7:
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 151 amino acids
? TYPE: AMINO ACID
? STANDARDS: single
? TOPOLOGY: linear
?
? FEATURE:
? NAME/KEY:
? LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION:
?
US-07-668-517-7

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Query Match	15.3%	Score 121;	DB 1;	Length 151;
Best Local Similarity	28.6%	Pred. No. 4.7e-07;		
Matches	44;	Conservative	21;	Mismatches 63;
			Indels	26;
			Gaps	6;

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QY 17 AHVISAASKETISVLOMAKEGYTTSNNLVLENNKQJTVRROGYLYIYAQVTF----- 70
Dd 7 AHVV--ANPQAEQOLQWLRNRRANLLANGVELRD--NQVVPSEGYLYIITSQVLFKGGQCP 63
QY 71 -----CSNRBSAOPFIASJCLSPCFERILLRANTSHSSKPCQGSIHJGV 12
Dd 64 STHVLLTHITISIANYSOTKNNULSAIISPCC-----RFPFGAEAKP--WTEPIYAGV 116
QY 122 FELQPGASVFNATDPQOVSHG--TGTFSPGLIKL 154
Dd 117 FOLEKGRLSAEINRPDYIDPAESQGVYEGIAL 150

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Search completed: June 7, 2003, 12:10:22  
Job time : 15 secs

Sat Jun '7 12:25:13 2003

us-09-579-548a-1\_108\_261.closed.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2003, 12:09:45 ; Search time 20 Seconds

(without alignments)  
794.950 Million cell updates/sec

Title: US-09-579-548a-1\_COPY\_108\_261

Perfect score: 792  
Sequence: 1 ENSFMQKGDNPQIAAHV.....TDPQSVSHGTGFTSGLLKL 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 178157

Minimum DB seq length: 0

Maximum DB seq length: 154

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.dep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.dep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.dep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.dep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.dep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.dep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.dep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	96.7	149	10	US-09-934-465-16
2	751	94.8	146	9	US-09-343-001-1
3	743	93.8	146	9	US-09-779-050A-10
4	546	68.9	146	9	US-09-779-050A-11
5	121	15.3	150	10	US-09-877-156-25
6	121	15.3	150	12	US-10-116-378-28
7	121	15.3	152	9	US-09-779-050A-9
8	112	14.1	149	10	US-09-934-465-17
9	110.5	14.0	151	9	US-09-779-050A-10
10	109.5	13.8	140	12	US-10-116-378-30
11	109.5	13.6	141	10	US-09-877-156-22
12	107.5	13.6	143	9	US-09-779-050A-7
13	107.5	13.6	143	9	US-09-779-050A-9
14	102.5	12.5	143	9	US-09-779-050A-8
15	94	11.9	18	9	US-10-272-411-28
16	86.5	10.9	149	9	US-09-779-050A-23
17	86	10.9	147	10	US-09-877-156-23
18	86	10.9	147	12	US-10-116-378-31
19	86	10.9	149	9	US-09-779-050A-22

20	84.5	10.7	102	9	US-09-779-050A-6	GENERAL INFORMATION
21	83	10.5	151	10	US-09-934-465-11	Sequence 11, Appl
22	77	9.7	144	9	US-09-779-050A-12	Sequence 12, Appl
23	77	9.7	145	10	US-09-877-156-21	Sequence 21, Appl
24	75	9.5	152	10	US-09-929-493-41	Sequence 41, Appl
25	73.5	9.3	104	9	US-10-045-574A-5	Sequence 5, Appl
26	73.5	9.3	104	10	US-09-911-777-5	Sequence 54, Appl
27	72	9.1	147	9	US-09-779-050A-13	Sequence 13, Appl
28	69	8.7	133	10	US-09-929-493-44	Sequence 44, Appl
29	67	8.5	109	9	US-10-045-574A-8	Sequence 8, Appl
30	67	8.5	109	10	US-09-911-777-8	Sequence 8, Appl
31	66	8.3	142	9	US-09-779-050A-27	Sequence 27, Appl
32	60	7.6	27	10	US-09-813-329-54	Sequence 54, Appl
33	60	7.6	27	10	US-09-813-329-64	Sequence 8, Appl
34	60	7.6	130	9	US-10-060-845-8	Sequence 8, Appl
35	60	7.6	130	12	US-10-072-159-8	Sequence 19, Appl
36	59	7.4	17	10	US-09-813-329-19	Sequence 20, Appl
37	59	7.4	17	10	US-09-813-329-20	Sequence 19, Appl
38	58.5	7.4	149	10	US-09-854-864-19	Sequence 41874, A
39	58.5	7.4	154	10	US-09-864-761-41874	Sequence 18, Appl
40	57	7.2	16	10	US-09-813-329-18	Sequence 4733, Ap
41	57	7.2	130	9	US-09-764-891-4733	Sequence 6, Appl
42	56	7.1	97	9	US-10-045-574A-6	Sequence 6, Appl
43	56	7.1	97	10	US-09-911-777-6	Sequence 878, App
44	56	7.1	135	9	US-09-925-299-878	Sequence 878, App
45	56	7.1	135	10	US-09-925-299-878	Sequence 878, App

#### ALIGNMENTS

RESULT 1  
US-09-934-465-16  
Sequence 16, Application US/09934465  
Patient No. US20020102233A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: Apo-2 LIGAND  
FILE REFERENCE: 11669.22US03  
CURRENT APPLICATION NUMBER: US/09/934,465  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 08/584,031  
PRIOR FILING DATE: 1996-01-09  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-934-465-16

Query Match 96.7%; Score 766; DB 10; Length 149;  
Best Local Similarity 100.0%; Pred. No. 1.9e-74;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	6	MOKGDPNPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLKNGKOLTVKROGIYYTY	65
DB	1	MOKGDPNPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLKNGKOLTVKROGIYYTY	60
QY	66	AQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGGOSIHLGVPFELQ	125
DB	61	AQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGGOSIHLGVPFELQ	120
QY	126	PGASVFNVTDPDPSOVSHGTGFTSGLLKL	154
DB	121	PGASVFNVTDPDPSOVSHGTGFTSGLLKL	149

RESULT 2  
US-09-343-001-1  
Sequence 1, Application US/09943001  
Publication No. US20030099642A1  
GENERAL INFORMATION:



```

; APPLICANT: Yellin, Michael J.
; APPLICANT: Iederman, Seth
; APPLICANT: Chess, Leonard
; TITLE OF INVENTION: THERAPEUTIC APPLICATIONS FOR THE
; TITLE OF INVENTION: ANTI-T-BAM (CD40-L) MONOCLONAL ANTIBODY 5c8
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/343,001
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/566,258
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 47279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278 0400
; TELEFAX: (212)391 0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-343-001-1

Query Match          94.8%; Score 751; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.6e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GDONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIYAQV 68
DB 1 GDONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIYAQV 60

QY 69 TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHLGVPFELQPGA 128
DB 61 TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHLGVPFELQPGA 120

QY 129 SVFVNTDPSQVSHGTFSTFGLLKL 154
DB 121 SVFVNTDPSQVSHGTFSTFGLLKL 146

RESULT 3
US-09-779-050A-10
; Sequence 10, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
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; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-10

Query Match          93.8%; Score 743; DB 9; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.5e-72;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GDONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIYAQV 68
DB 1 GDONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIYAQV 60

QY 69 TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHLGVPFELQPGA 128
DB 61 TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHLGVPFELQPGA 120

QY 129 SVFVNTDPSQVSHGTFSTFGLLKL 154
DB 121 SVFVNTDPSQVSHGTFSTFGLLKL 146

RESULT 4
US-09-779-050A-11
; Sequence 11, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-779-050A-11

Query Match          68.9%; Score 546; DB 9; Length 146;
Best Local Similarity 74.0%; Pred. No. 7.1e-51;
Matches 108; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 9 GDONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIYAQV 68
DB 1 GDONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIYAQV 60

QY 69 TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHLGVPFELQPGA 128
DB 61 TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHLGVPFELQPGA 120

QY 129 SVFVNTDPSQVSHGTFSTFGLLKL 154
DB 121 SVFVNTDPSQVSHGTFSTFGLLKL 146

RESULT 5
US-09-877-156-25
; Sequence 25, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
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Db 9 AHUTGKNSRSMPL-EMED-----TYGIVLISGVKKKGGVLNATGTYFYVSKYFFRG 61  
QY 71 --CSNREASSQAFLIASLCLKSPGRFERILLRAANTHSSAKPCGQ---OSIHIGVFEIQ 125  
Db 62 OSCNN-----LPLSHKVYMRN-SKYPQDLVMEEGKQMSYCTTGQWMASSYLGAVFNL 114  
QY 126 PGASVFVNVTPDSQVSHGTGFTSPGLKL 154  
Db 115 SADHLVNVSELSLVNFEESQTFPGLYKL 143

RESULT 13  
US-09-779-050A-9  
; Sequence 9, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 143  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-09-779-050A-9

Query Match 13.6%; Score 107.5; DB 9; Length 143;  
Best Local Similarity 26.2%; Pred. No. 0.00069;  
Matches 39; Conservative 30; Mismatches 67; Indels 13; Gaps 7;

QY 11 QNPQIAAHVISEASKTSVLOWAEKGYTMSNNLVTLENGKQLTVKQGLYTYAQT 70  
Db 3 KKRPSVAHLTGPNRSRIP-LEW-EDTYGTALISGVKTKG-GLVINEAGLYFYVSKYVF 59  
QY 71 ---CSNREASSQAFLIASLCLKSPGRFERILLRAAN-THSSAKPCGQOSIHIGVFEIQ 125  
Db 60 RGQSCNNSQPLSHK--VYMRNFKYPG--DLVMEKKINCYCTTGQIWAHSSYLGAVFNL 114  
QY 126 PGASVFVNVTPDSQVSHGTGFTSPGLKL 154  
Db 115 SADHLVNVSELSLVNFEESQTFPGLYKL 143

RESULT 14  
US-09-779-050A-8  
; Sequence 8, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 143  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-779-050A-8

Query Match 12.9%; Score 102.5; DB 9; Length 143;  
Best Local Similarity 25.5%; Pred. No. 0.0024;  
Matches 39; Conservative 25; Mismatches 68; Indels 21; Gaps 6;

QY 11 QNPQIAAHVISEASKTSVLOWAEKGYTMSNNLVTLENGKQLTVKQGLYTYAQT 70  
Db 3 KKRPSVAHLTGPNRSRIP-LEW-EDTYGTALISGVKTKG-GLVINEAGLYFYVSKYVF 59  
QY 71 ---CSNREASSQAFLIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHIGV 121  
Db 60 RGQSCNNSQPLSHK--VYMRNFKYPG--DLVMEKKINCYCTTGQIWAHSS-----YLGA 110  
QY 122 FELQPGASVFVNVTPDSQVSHGTGFTSPGLKL 154  
Db 111 FNLTSADHLVNVISQLINFEESKTFPGLYKL 143

RESULT 15  
US-10-272-411-28  
; Sequence 28, Application US/10272411  
; Publication No. US20030100068A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Ross, P. Patrick  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0202  
; CURRENT APPLICATION NUMBER: US/10/272,411  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/329,393  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-411-28

Query Match 11.9%; Score 94; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EASKTSVLOWAEKGY 39  
Db 1 EASKTSVLOWAEKGY 18

Search completed: June 7, 2003, 12:15:52  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2003, 12:04:41 ; Search time 69 Seconds  
(without alignments)  
297.400 Million cell updates/sec

Title: US-09-579-548a-1\_COPY\_108\_261

Perfect score: 792  
Sequence: 1 ENSPEKQKDQNPQIAAHVI.....TPDSQVSHGTGFTSPGLMKI 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 659595

Minimum DB seq length: 0

Maximum DB seq length: 154

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*

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2: /SID22/gcgcdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SID22/gcgcdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SID22/gcgcdata/geneseq/geneseq-emb1/AA1983.DAT:\*

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22: /SID22/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SID22/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	751	94.8	146	18	AAW24936
2	751	94.8	146	18	AAW24555
3	751	94.8	146	21	AAW24555
4	721	91.0	141	22	AAW24555
5	648	81.8	125	16	AAW24555
6	558	70.5	146	21	AAW24555
7	139	17.6	139	21	AAW24555
8	130	16.4	152	22	AAW24555
9	127	16.0	154	13	AAW24555
10	123.5	15.6	150	9	AAW24555

11	123.5	15.6	150	9	AAW24555
12	123	15.5	150	15	AAW24555
13	123	15.5	151	12	AAW24555
14	123	15.5	151	12	AAW24555
15	122.5	15.5	150	13	AAW24555
16	122.5	15.5	154	6	AAW24555
17	122.5	15.5	154	6	AAW24555
18	122.5	15.5	154	6	AAW24555
19	122.5	15.5	154	11	AAW24555
20	122	15.4	150	12	AAW24555
21	122	15.4	151	12	AAW24555
22	122	15.4	152	13	AAW24555
23	122	15.4	152	21	AAW24555
24	121.5	15.3	154	11	AAW24555
25	121.5	15.3	154	11	AAW24555
26	121	15.3	147	9	AAW24555
27	121	15.3	147	22	AAW24555
28	121	15.3	147	22	AAW24555
29	121	15.3	149	10	AAW24555
30	121	15.3	150	8	AAW24555
31	121	15.3	150	8	AAW24555
32	121	15.3	150	9	AAW24555
33	121	15.3	150	9	AAW24555
34	121	15.3	150	9	AAW24555
35	121	15.3	150	10	AAW24555
36	121	15.3	150	11	AAW24555
37	121	15.3	151	9	AAW24555
38	121	15.3	151	9	AAW24555
39	121	15.3	151	10	AAW24555
40	121	15.3	151	11	AAW24555
41	121	15.3	151	12	AAW24555
42	121	15.3	151	12	AAW24555
43	121	15.3	151	12	AAW24555
44	121	15.3	151	12	AAW24555
45	121	15.3	152	9	AAW24555

#### ALIGNMENTS

RESULT 1	AAW24936	standard; protein; 146 AA.
ID	AAW24936	standard; protein; 146 AA.
AC	AAW24936	
DT	13-FEB-1998	(first entry)
DE	Anti-CD40L monoclonal antibody 5c8.	
DE	Anti-CD40L monoclonal antibody; Mab; inhibition; CD40 ligand;	
KW	arthritis; viral infection; autoimmune disease; fibroblast cell;	
KW	fibrosis; cirrhosis; multiple myeloma.	
XX		
OS	Murine sp.	
XX		
PN	WO9720063-A1.	
XX		
PD	05-JUN-1997.	
XX		
PF	27-NOV-1996;	96WO-US19172.
XX		
PR	22-APR-1996;	96US-0637323.
PR	01-DEC-1995;	95US-0566258.
XX	01-DEC-1995;	95US-0567391.
PA	(BIOJ ) BIOGEN INC.	
PA	(UYCO ) UNIV COLUMBIA NEW YORK.	
XX		
PI	Chess L, Karpusas MN, Lederman S, Thomas DW, Yellin MJ;	
XX		
DR	WPI, 1997-310616/28.	
XX		

TNF analogue. AA  
Human TNF mutein.  
Tumour Necrosis Fa  
Tumour Necrosis Fa  
TNF polypeptide mu  
Sequence of a pure  
Rabbit tumor necro  
TNF analogue havin  
Rabbit tumor necr  
Tumour Necrosis Fa  
Tumour Necrosis Fa  
Tumour necrosis fa  
Amino acid sequenc  
Tumoricidal polype  
Tumoricidal polype  
Sequence of modifi.  
Human tumour necro  
C-terminal region  
Polypeptide derive  
Synthetic tumour n  
TNF-derived polype  
Modified tumour ne  
Sequence of new ph  
Sequence of new ph  
Anti-tumour active  
New polypeptide wi  
Anti-tumour peptid  
Sequence of modifi  
Polypeptide with a  
Anti-tumour peptid  
Tumour Necrosis Fa  
Tumour Necrosis Fa  
Tumour necrosis fa  
Human TNF with mod  
Anti-tumour polype

PT Inhibition of activation of cells bearing CD40 - used for inhibiting  
PT an inflammatory response or treating e.g. arthritis, fibrosis,  
PT auto-immune diseases or multiple myeloma  
PS Claim 23; Page 82; 145pp; English.  
XX  
CC This is an anti-CD40L monoclonal antibody 5c8. It is used in a method  
CC for inhibiting interaction between cells bearing CD40 on their cell  
CC surface and CD40 ligand which activates the cells. The cells are  
CC contacted with this protein which inhibits the binding of CD40 ligand to  
CC CD40 on the cells, thereby inhibiting activation of the cells. This  
CC protein is a Fab or a single chain antibody comprising the soluble  
CC extracellular region of CD40 or its ligand. The protein comprises an  
CC IgA1, IgA2, IgG1, IgG2, IgG3, IgG4, IgM, IgD or IgE Fc region capable of  
CC binding to protein A or G fused to the CD40 extracellular region. The  
CC method can be used for inhibiting an inflammatory response or treating  
CC conditions dependent on CD40 ligand-induced activation of fibroblast  
CC cells, such as rheumatoid arthritis, non-rheumatoid inflammatory  
CC arthritis, osteoarthritis, pulmonary fibrosis secondary to adult  
CC respiratory distress syndrome, drug-induced pulmonary fibrosis,  
CC fibrotic disease of the liver such as hepatitis, cirrhosis, viral  
CC infection or autoimmune disease. The methods can also be used for  
CC treating multiple myeloma and conditions dependent on CD40 ligand-induced  
CC activation of endothelial cells such as atherosclerosis, reperfusion  
CC injury, allograft or organ rejection.  
XX  
SQ Sequence 146 AA;  
XX  
Query Match 94.8%; Score 751; DB 18; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2.4e-75;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 GDONPQIAAHVISEASKTTSTVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYTYAQQV 68  
DB 1 GDONPQIAAHVISEASKTTSTVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYTYAQQV 60  
QY 69 TFCSNREASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHGQVFELOPGA 128  
DB 61 TFCSNREASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHGQVFELOPGA 120  
QY 129 SVFVNVTPDSQVSHGTFSPGLKL 154  
DB 121 SVFVNVTPDSQVSHGTFSPGLKL 146  
XX  
RESULT 2  
AAW24555  
ID AAW24555 standard; protein; 146 AA.  
XX  
AC AAW24555;  
XX  
DT 28-JAN-1998 (first entry)  
XX  
DE Soluble extracellular fragment of human CD40 ligand (residues 116-261).  
XX  
KW CD40 ligand; inflammatory kidney disease; renal tubule; renal cell;  
KW autoantibody deposition; glomerulonephritis; CD40-positive.  
XX  
OS Homo sapiens.  
XX  
PN WO9726000-A1.  
XX  
PD 24-JUL-1997.  
XX  
PF 16-JAN-1997; 97WO-US00668.  
XX  
XX 16-JAN-1997;  
XX  
PR 01-MAY-1996; 96US-0641473.  
PR 16-JAN-1996; 96US-0587334.  
XX  
PA (BIO) BIOGEN INC.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
XX  
PI Chess L, Karpusas MN, Lederman S, Thomas DW, Yellin MJ;

XX  
DR WPI; 1997-385109/35.  
XX  
PT Inhibiting ligand-induced activation of CD40-positive renal cells -  
PT with agent that prevents ligand-CD40 interaction, for treating a  
PT wide variety of inflammatory kidney diseases  
XX  
PS Disclosure; Page 38; 83pp; English.  
XX  
CC The present sequence represents the known extracellular fragment of human  
CC CD40 ligand. A novel method for inhibiting the activation by CD40 ligand  
CC of renal cells having CD40 on their surface, comprises treating the cells  
CC with an agent that inhibits interaction between CD40 and its ligand.  
CC This method is useful in human and veterinary medicine to treat a very  
CC wide range of inflammatory kidney diseases, e.g. those not initiated by  
CC autoantibody deposition, glomerulonephritis and diseases affecting renal  
CC tubules.  
XX  
SQ Sequence 146 AA;  
XX  
Query Match 94.8%; Score 751; DB 18; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2.4e-75;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 GDONPQIAAHVISEASKTTSTVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYTYAQQV 68  
DB 1 GDONPQIAAHVISEASKTTSTVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYTYAQQV 60  
QY 69 TFCSNREASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHGQVFELOPGA 128  
DB 61 TFCSNREASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHGQVFELOPGA 120  
QY 129 SVFVNVTPDSQVSHGTFSPGLKL 154  
DB 121 SVFVNVTPDSQVSHGTFSPGLKL 146  
XX  
RESULT 3  
AAB08268  
ID AAB08268 standard; Protein; 146 AA.  
XX  
AC AAB08268;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE Amino acid sequence of a human TNF ligand CD40L.  
XX  
KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
KW type II transmembrane protein; B cell stimulatory factor;  
KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
KW lupus and graft versus host disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200047740-A2.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US03653.  
XX  
XX 12-FEB-1999; 99US-0119906.  
PR 18-NOV-1999; 99US-0166271.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Boyle WJ, Hsu H;  
XX  
DR WPI; 2000-558217/51.  
XX  
PT Novel polypeptides comprising tumour necrosis factor ligand family  
PT proteins, useful for treating inflammatory and immune disorders, e.g.  
PT rheumatoid arthritis -

PS Claim 14; Fig 9; 71pp; English.  
XX  
CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
CC specification describes an AGP-3 polypeptide, which is TNF ligand  
CC family member. AGP-3 is a type II transmembrane protein, and is a  
CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
CC increases in the number of B cells and immunoglobulins produced.  
CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
CC Crohn's disease, lupus and graft versus host disease. The nucleic  
CC acids may be used to regulate the expression of an AGP-3 related  
CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
CC useful for the detection of AGP-3 agonists, antagonists and  
CC characterizing interactions with AGP-3 related proteins.  
XX  
SQ Sequence 146 AA;  
  
Query Match 94.8%; Score 751; DB 21; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2.4e-75;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 GDQNPQIAAHVISEASSTKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGLYTYIAOV 68  
DB 1 GPQNPQIAAHVISEASSTKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGLYTYIAOV 60  
QY 69 TFCNSREASQAFLASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHLGCVFELQPGA 128  
DB 61 TFCNSREASQAFLASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHLGCVFELQPGA 120  
QY 129 SYFVNVTPDSQVSHGTGFTSFGLLKL 154  
DB 121 SYFVNVTPDSQVSHGTGFTSFGLLKL 146  
  
RESULT 4  
AAB67246  
ID AAB67246 standard; protein; 141 AA.  
XX  
AC AAB67246;  
XX  
DT 18-APR-2001 (first entry)  
XX  
DE Human CD40L.  
XX  
KM Human; Apo2 ligand; divalent metal ions; viral infection; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200100832-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 26-JUN-2000; 2000WO-US17579.  
XX  
PR 28-JUN-1999; 99US-0141342.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;  
PI O'Connell M, Pai R, Shahrokhi Z, Simmons L;  
XX  
DR WPI; 2001-123012/13.  
XX  
PT Use of divalent metal ions for making Apo-2 ligand and in formulations  
PT containing Apo-2 ligand for increasing yield and stability of ligand  
PT trimers, useful for therapeutic applications -  
XX  
PS Disclosure; Fig 3; 60pp; English.  
XX  
CC The present invention relates to a formulation comprising Apo-2  
CC ligand and divalent metal ions. Apo-2 ligand and the formulation  
CC are useful for treating cancers and viral infections. Addition  
CC of divalent metal ions for making Apo-2 ligand and formulations

CC containing Apo-2 ligand results in increased yield and stability  
CC of Apo-2 ligand trimers.  
XX  
SQ Sequence 141 AA;  
  
Query Match 91.0%; Score 721; DB 22; Length 141;  
Best Local Similarity 100.0%; Pred. No. 4.9e-72;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 14 QIAAHVISEASSTKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGLYTYIAOVFCSN 73  
DB 1 QIAAHVISEASSTKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGLYTYIAOVFCSN 60  
QY 74 REASQAAPFLASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHLGCVFELQPGASVFN 133  
DB 61 REASQAAPFLASLCLKSPGRPERILLRAANTHSSAKPCGQOSIHLGCVFELQPGASVFN 120  
QY 134 VTPDSQVSHGTGFTSFGLLKL 154  
DB 121 VTPDSQVSHGTGFTSFGLLKL 141  
  
RESULT 5  
AAR80838  
ID AAR80838 standard; Protein; 125 AA.  
XX  
AC AAR80838;  
XX  
DT 28-FEB-1996 (first entry)  
XX  
DE Human CD40 ligand exon 5 protein sequence.  
XX  
KM Exon; intron; chromosome; human CD40 ligand; PCR; amplification; primer;  
KM probe; antisense; gene therapy; HIV syndrome.  
XX  
OS Homo sapiens.  
XX  
PN JP07163362-A.  
XX  
PD 27-JUN-1995.  
XX  
PF 25-NOV-1993; 93JP-0295102.  
XX  
PR 21-OCT-1993; 93JP-0263258.  
XX  
PA (MITP ) MITSUBISHI YUKA BCL KK.  
XX  
DR WPI; 1995-260044/34.  
XX  
DR N-PSDB; AAT05794.  
XX  
PT Novel chromosomal DNA encoding a CD40 ligand and probes - useful for  
PT diagnosis and gene therapy of HIV syndrome.  
XX  
PS Claim 1; Page 7-8; 14pp; Japanese.  
XX  
CC The amino acid sequence encoded by exon 5 of the chromosomal DNA  
CC sequence encoding the human CD40 ligand. This sequence corresponds to  
CC residues 139-264 of the CD40 ligand. The gene was isolated using an  
CC amplified fragment of the gene as a probe. The probe was a fragment  
CC amplified by the primers AAQ99758-9. The CD40 ligand primary gene is  
CC approx. 11 kb long and consists of 5 exons and 4 intron sequences  
CC (AAQ9790-4). The sequence of the coding region was used to design a set  
CC of oligonucleotides (AAQ9760-73) which can be used as antisense probes  
CC for use in diagnosis and gene therapy of HIV syndrome.  
XX  
SQ Sequence 125 AA;  
  
Query Match 81.8%; Score 648; DB 16; Length 125;  
Best Local Similarity 100.0%; Pred. No. 5.4e-64;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 30 VLOMAEKGYTMSNNLVTLENGKQLTVKRGOLYTYIAOVFCNSREASQAAPFLASLCLK 89  
|||||

Db 1 VLQWAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQVTFCSNREASSQAPFLASLCLK 60  
 QY 90 SCGRFERILLRAANTHSSAKPCGQOSIHIGVFELOPGASVYVNTDPSQVSHGTFSTF 149  
 Db 61 SCGRFERILLRAANTHSSAKPCGQOSIHIGVFELOPGASVYVNTDPSQVSHGTFSTF 120  
 QY 150 GLLKL 154  
 Db 121 GLLKL 125

RESULT 6  
 AAB08269  
 ID AAB08269 standard; Protein; 146 AA.  
 XX  
 AC AAB08269;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX

DE Amino acid sequence of a mouse TNF ligand GP40L.  
 XX  
 KM AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KM type II transmembrane protein; B cell stimulatory factor;  
 KM inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KM lupus and graft versus host disease.  
 XX

OS Mus sp.  
 XX WO200047740-A2.  
 XX PD 17-AUG-2000.  
 XX PF 11-FEB-2000; 2000WO-US03653.  
 XX PR 12-FEB-1999; 99US-0119906.  
 PR 18-NOV-1999; 99US-0166271.  
 XX (AMGE-) AMGEN INC.  
 PA Boyle WJ, Hsu H;  
 PI  
 XX WPI; 2000-558217/51.  
 DR

PT Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 XX  
 PS Claim 14; Fig 9; 71pp; English.  
 XX

CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
 CC

XX Sequence 146 AA;

Query Match 70.5%; Score 558; DB 21; Length 146;  
 Best Local Similarity 74.7%; Pred. No. 6.7e-54;  
 Matches 109; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 9 GDNQPIAAHVTSSEASKTTSVLOWAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQV 68  
 Db 1 GDDPPIAAHVTSSEASKTTSVLOWAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQV 60  
 QY 69 TFCSNREASSQAPFLASLCLKSGRFERILLRAANTHSSAKPCGQOSIHIGVFELOPGA 128

Db 61 TFCSNREASSQAPFLASLCLKSGRFERILLRAANTHSSAKPCGQOSIHIGVFELOPGA 120  
 QY 129 SVFNVVTPDSQVSHGTFSTFGLKL 154  
 Db 121 SVFNVVTPDSQVSHGTFSTFGLKL 146

RESULT 7  
 AAY91023  
 ID AAY91023 standard; Protein; 139 AA.  
 XX  
 AC AAY91023;  
 XX  
 DT 05-SEP-2000 (first entry)  
 XX

DE Mouse OBM protein sequence SEQ ID NO:8.  
 XX

KM Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF;  
 KM OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH;  
 KM parathyroid hormone.  
 XX

OS Mus sp.  
 XX JP2000102390-A.  
 XX PD 11-APR-2000.  
 XX PF 30-SEP-1998; 98JP-0292971.  
 XX PR 30-SEP-1998; 98JP-0292971.  
 XX

PA (SNOW) SNOW BRAND MILK PROD CO LTD.  
 PA (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.  
 XX  
 DR WPI; 2000-332087/29.  
 DR N-PSDB; AAA39155.  
 XX

PT A DNA and preparation of a protein by using it -  
 PT  
 XX  
 PS Example 2; Page 14; 18pp; Japanese.  
 XX

CC The present invention describes a genomic DNA encoding a protein having  
 CC an activity of supporting or promoting differentiation and maturation of  
 CC osteoclasts. The genomic DNA encoding a protein has the following  
 CC properties: (a) combines specifically with osteoclastogenesis inhibitory  
 CC factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)  
 CC of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide  
 CC gel electrophoresis) under a nonreductive condition and the apparent mw  
 CC when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c)  
 CC has an activity of supporting or promoting differentiation and maturation  
 CC of osteoclast in the co-culture of mouse osteoblast-like stroma cell and  
 CC mouse spleen cell in the presence of a bone absorption promoting factor  
 CC such as active type vitamin D3 and parathyroid hormone (PTH). The protein  
 CC can be used as a drug and a research reagent. The present sequence  
 CC represents a mouse OCIF binding molecule (OBM) from the present  
 CC invention.  
 CC

XX Sequence 139 AA;

Query Match 17.6%; Score 139; DB 21; Length 139;  
 Best Local Similarity 29.1%; Pred. No. 2.3e-07;  
 Matches 41; Conservative 26; Mismatches 58; Indels 16; Gaps 6;

QY 24 SKTTSVLOWAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQVTFCSNREASSQAP-- 81  
 Db 1 SHKVTLSWYHDRCWAKISN--MTLSNGK-LRVNODGYIYANICF-RHHTSGSVPTD 56  
 QY 82 -----FLASLCLKSGRFERILLRAANTH--SSAKPCGQOSIHIGVFELOPGASVFN 133  
 Db 57 YLOLMVYVVKTSIKIPSSHN--LNMGSTKWSGNSSEPHFYSINVGGFKLRAGEISIQ 114  
 QY 134 VTPDSQVSHGTFSTFGLKL 154



Db 115 VSNPSLDDPDODATYFGAFKV 135

## RESULT 8

AAB67248 standard; protein; 152 AA.

AC AAB67248;

DT 18-APR-2001 (first entry)

DE Human RANKL.

KW Human; Apo2 ligand; divalent metal ions; viral infection; cancer.

OS Homo sapiens.

PN MO200100832-A1.

PD 04-JAN-2001.

PF 26-JUN-2000; 2000MO-US17579.

PR 28-JUN-1999; 99US-0141342.

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;

PI O'Connell M, Pai R, Shahrokh Z, Simmons L;

DR WPI; 2001-123012/13.

PT Use of divalent metal ions for making Apo-2 ligand and in formulations

PT containing Apo-2 ligand for increasing yield and stability of ligand

PT trimers, useful for therapeutic applications.

PS Disclosure; Fig 3; 60pp; English.

CC The present invention relates to a formulation comprising Apo-2

CC ligand and divalent metal ions. Apo-2 ligand and the formulation

CC are useful for treating cancers and viral infections. Addition

CC of divalent metal ions for making Apo-2 ligand and formulations

CC containing Apo-2 ligand results in increased yield and stability

CC of Apo-2 ligand trimers.

CC

CC

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CC

DE TNF polypeptide mutein, lacking residue 106.

KW Tumour necrosis factor; anti-tumour; metastasis; cancer; melanoma;

KW leukaemia.

OS Homo sapiens.

PN EP477791-A.

PD 01-APR-1992.

PF 20-SEP-1991; 91EP-0116017.

PR 17-JUN-1991; 91JP-0240131.

PR 21-SEP-1990; 90JP-0250046.

PA (ISHH ) ISHIMURA SANGYO KAISHA.

PI Yamada N, Kato M, Miyata K, Aoyama Y, Shikama H;

PI WPI; 1992-106202/14.

PT New Tumour Necrosis Factor polypeptide mutein - useful in

PT treating solid tumours e.g. colorectal, lung, gastric and

PT pancreatic cancers, without promoting tumour metastasis

PS Claim 1; Page 35; 55pp; English.

CC The protein sequence was obtd. from a synthetic cDNA sequence based

CC on the human TNF sequence. The synthetic DNA was used to transform E.

CC coli cells, and the mutein purified by standard chromatography. The

CC polypeptide is a human TNF N-terminal mutein contg. a deletion at

CC residue 106 and having anti-tumour effects similar to those of human

CC TNF but lacking its side effect of promoting metastasis. It can be

CC used as the active agent in compns. pref. to treat solid tumours

CC such as colorectal, lung, gastric and pancreatic cancer, and melanoma

CC and leukaemia.

CC See also AAR22303-16 and AAR22721-5.

CC

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CC

DE TNF polypeptide mutein, lacking residue 106.

KW Tumour necrosis factor; anti-tumour; metastasis; cancer; melanoma;

KW leukaemia.

OS Homo sapiens.

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CC The protein sequence was obtd. from a synthetic cDNA sequence based

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CC coli cells, and the mutein purified by standard chromatography. The

CC polypeptide is a human TNF N-terminal mutein contg. a deletion at

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CC and leukaemia.

CC See also AAR22303-16 and AAR22721-5.

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KW Tumour necrosis factor; anti-tumour; metastasis; cancer; melanoma;

KW leukaemia.

OS Homo sapiens.

PN EP477791-A.

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PR 17-JUN-1991; 91JP-0240131.

PR 21-SEP-1990; 90JP-0250046.

PA (ISHH ) ISHIMURA SANGYO KAISHA.

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PT pancreatic cancers, without promoting tumour metastasis

PS Claim 1; Page 35; 55pp; English.

CC The protein sequence was obtd. from a synthetic cDNA sequence based

CC on the human TNF sequence. The synthetic DNA was used to transform E.

CC coli cells, and the mutein purified by standard chromatography. The

CC polypeptide is a human TNF N-terminal mutein contg. a deletion at

CC residue 106 and having anti-tumour effects similar to those of human

CC TNF but lacking its side effect of promoting metastasis. It can be

CC used as the active agent in compns. pref. to treat solid tumours

CC such as colorectal, lung, gastric and pancreatic cancer, and melanoma

CC and leukaemia.

CC See also AAR22303-16 and AAR22721-5.

CC

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CC

XX 23-APR-1987; 87JP-0098552.  
 PF XX  
 XX 23-APR-1987; 87JP-0098552.  
 PR XX  
 XX (TEIJ ) TEIJIN KK.  
 PA XX  
 XX  
 DR WPI; 1988-357026/50.  
 DR N-PSDB; AAN82096.  
 XX  
 PT New physiologically active polypeptide - is different from known  
 PT human TNF protein and has antitumour activity.  
 XX  
 PS Claim 1; Page 1; 18pp; Japanese.  
 XX  
 CC This physiologically active peptide is produced using recombinant DNA  
 CC methods and is useful as an antitumour agent. It is applied as a  
 CC drug compn. See also J63267291.  
 XX  
 XQ Sequence 150 AA;

```

Query Match      15.6%  Score 123.5  DB 9;  Length 150;
Best Local Similarity 29.4%  Pred. No. 14e-05;
Matches 45;  Conservative 23;  Mismatches 60;  Indels 25;  Gaps 7;

QY 17 AHVISEASKTTSTVLOMAEKGYVTWNNLVTLENGKOLTVKRGQGYTYAQTFF-----CS 72
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 8 AHVV--ANPQAEQGLQWLNRRRANMLANGVELRD--NQLVPSREGIYLILYSVLFGGGQGP 64
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 73 -----NREASSQAPFIASLCCKSPGRFETILLRPAANTHSSAKPCGQOOSIHLGVF 122
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 65 STHVLLTHTTISRIAVSYQTKVNLMSAIKSPQ-----RETPEGAKAK--WTEPIILGVF 117
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 123 ELQPGASVFVNVTPDSQVSHG--TGFTSGGLKL 154
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 118 QLEKGDRIASAEINRPDYLDFAESGGVYFGIALL 150
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

RESULT 11  
ID AAP82303 standard; protein, 150 AA.  
AC AAP82303;  
XX  
DT 15-NOV-1990 (first entry)  
XX  
DE TNF analogue.  
XX  
TNF; drug compsn.  
XX  
PN JP63267290-A.  
XX  
PD 04-NOV-1988.  
XX  
PF 23-APR-1987; 87JP-0098552.  
XX  
PR 23-APR-1987; 87JP-0098552.  
XX  
PA (TEIJ ) TEIJIN KK.  
XX  
DR WPI; 1988-357026/50.  
DR N-PSDB; AAN82098.  
XX  
XX  
New physiologically active polypeptide - is different from known  
human TNF protein and has antitumour activity.  
PT  
PT  
XX  
Claim 1; Page 1; 18pp; Japanese.  
PS

CC This physiologically active peptide is produced using recombinant DNA  
CC methods and is useful as an antitumour agent. It is applied as a  
CC drug compsn. See also J63267290.  
XX  
Sequence 150 AA;

```

Query Match      15.6%  Score 123.5  DB 9  Length 150;
Best Local Similarity 29.4%  Pred 1.4e-05;
Matches 45; Conservative 23; Mismatches 60; Indels 25; Gaps 7

QY 17 AHVISEASKTTSYLQMAEKGYTMSNNLVLTLENGKQLTVRKGLYYIYAQTF-----CS 72
    |||  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -
Db 8 AHVV-ANPQAGEGQWLNRRANMALANGVELRD-NQLVVSEGLYLYISQVLFPGQGCP 64
    |||  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -

QY 73 -----NRASSQAPFIASLCLKSPGFERILLPAANTHSSAKKCGQOOSIHLGVF 122
    |||  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -
Db 65 STHVLLHTTISRIAVSQYTKNALSPAIKPCQ-----RETPEGAFAKP-WYEPIYLGVF 117
    |||  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -

QY 123 ELQPGASVFVNVTDPGQVSHG-TGFTSGLLKL 154
    |||  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -
Db 118 QLEKQDRLSAELNRPDIYLDPAESQGVYTGIIAL 150
    |||  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -

```

XX	RESULT 12
XX	AAR69583
XX	ID AAR69583 standard; Protein, 150 AA.
XX	AC AAR69583;
XX	DT 13-MAR-1995 (first entry)
XX	DE Human TNF mutein.
XX	XX Tumour necrosis factor; TNF; mutein; variant; antitumour;
KW	toxicity; haemorrhagic necrosis; antiviral; parasite; malaria.
XX	OS Homo sapiens.
XX	DE4404124-A.
XX	PD 11-AUG-1994.
XX	PP 09-FEB-1994; 94DE-4404124.
XX	PR 09-FEB-1993; 93KR-0001751.
XX	PA (HANI-) HANIL SYNTHETIC FIBER CO LTD.
XX	PI Kang S, Lee I, Shin H-C, Shin N-K;
XX	WP1; 1994-250457/31.
XX	PT New tumour necrosis factor muteins and related DNA - also vectors
PT	and transformed cells, with increased antitumour activity and
PT	lower toxicity than wild type protein
XX	Claim 4 and 9; Page 20-21; 23pp; German.
XX	TNF muteins are claimed, in which at least one amino acid at
CC	positions 4-10, 38-41, 52-54, 56, 85-88, 127-129, 156 or 157 is
CC	exchanged for a different amino acid. Opt. one or more of the first
CC	7 N-terminal amino acids is deleted. TNF causes haemorrhagic
CC	necrosis of tumours; has anti-viral activity and inactivates some
CC	species of malarial parasites. The muteins have increased antitumour
CC	activity and lower toxicity than wild-type protein.
CC	The sequence given below is of a TNF mutein having Tyr87 replaced by
CC	Glu and the first 7 amino acids are deleted.
CC	Any TNF mutein may have an additional N-terminal Met residue,
CC	if expressed in E.coli.
XX	Sequence 150 AA;
XX	IQ

	Query Match	15.5%	Score 123;	DB 15;	Length 150;
	Best Local Similarity	28.6%;	Pred. No. 1.se-05;		
	Matches 44;	Conservative 21;	Mismatches 63;	Indels 26;	Gaps 6,
Oy	17 AHYISEASSKTTSVQLWAEGKYTMMNLVTLENGKRLTYKRQSLYYIYAQVP-----	70			
	:   : :	:	:	:     :	

Db 7 AHVV--ANPQAEGLQWLNRRANALLANGVELRD-NQLVVPSSEGLYLYISQVLFKGGGCP 63  
 QY 71 -----CSNFBASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGCGQSIHLGAV 121  
 Db 64 STHVLLTHRTISRIASVEQTKVNLISAIKSPCQ-----RETPEGAEAKP-WYEPIYIGGV 116  
 QY 122 FELQPGASVFVNVTDPDSQVSHG--TGFTSFGLLKL 154  
 Db 117 FOLEKGRLSAEINRPDYLDFAESGQVYFGIIAL 150

RESULT 13  
 AAR11615  
 ID AAR11615 standard; Protein; 151 AA.

XX AAR11615;  
 AC AAR11615;  
 XX 19-JUN-1991 (first entry)  
 DT Tumour Necrosis Factor analogue.  
 XX  
 DE Tumour Necrosis Factor analogue.  
 XX  
 KM TNF; anti-tumour agent; plasmid PTNF609.  
 XX  
 PN JP03058793-A.  
 XX  
 PD 13-MAR-1991.  
 XX  
 PF 27-JUL-1989; 89JP-0192488.  
 XX  
 PR 27-JUL-1989; 89JP-0192488.  
 XX  
 PA (TEIJD ) TEIJIN KK.  
 DR WPI; 1991-120507/17.  
 DR N-PSDB; AAQ11488.  
 XX  
 PT Physiologically active polypeptide different from human TNF -  
 PT prep'd. by culturing recombinant microbial cell to produce  
 PT polypeptide  
 XX  
 PS Claim 2; Page 1; 22pp; Japanese.  
 XX  
 CC The sequence is a derivative of human TNF. It is encoded by  
 CC plasmid pTNF609 which is transformed into E.coli for production of  
 CC the TNF analogue, which may or may not carry an N-terminal Met. The  
 CC analogue is effective against tumours.  
 CC Related patents are J03061495 and J03058795.  
 CC  
 XX  
 SQ Sequence 151 AA;

Query Match 15.5%; Score 123; DB 12; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 1.6e-05;  
 Matches 46; Conservative 21; Mismatches 66; Indels 28; Gaps 7;

QY 10 DONPOIAHAVISSEASKTTSVLQMAEKGYTMSNNLVTLLENGKQLTVKRGGLYTYAQT 69  
 Db 3 DDKP--VAHV--ANPQAEGLQWLNRRANALLANGVELRD-NQLVVPSSEGLYLYISQVL 57  
 QY 70 F-----CSNFBASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGCGQ 114  
 Db 58 FKGGCGPSTHVLLTHRTISRIASVEQTKVNLISAIKSPCQ-----RETPEGAEAKP-WYE 110  
 QY 115 SIHLGVPFELQPGASVFVNVTDPDSQVSHG--TGFTSFGLLKL 154  
 Db 111 PIYIGVFOLEKGRLSAEINRPDYLDFAESGQVYFGIIAL 151

RESULT 14  
 AAR11968  
 ID AAR11968 standard; Protein; 151 AA.  
 XX  
 AC AAR11968;  
 XX

DT 25-JUL-1991 (first entry)  
 XX  
 DE Tumour Necrosis Factor analogue.  
 XX  
 KM TNF; anti-tumour agent; PTNF604; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP03087197-A.  
 XX  
 PD 11-APR-1991.  
 XX  
 PF 31-AUG-1989; 89JP-0223222.  
 XX  
 PR 31-AUG-1989; 89JP-0223222.  
 XX  
 PA (TEIJD ) TEIJIN KK.  
 XX  
 DR WPI; 1991-152433/21.  
 DR N-PSDB; AAQ11703.  
 XX  
 PT New TNF-analogue polypeptide - useful as antitumour agent  
 PS  
 PS Claim 1; Page 1; 23pp; Japanese.  
 XX  
 CC The Met residue at position 1 can be absent from the protein without  
 CC affecting anti-tumour activity. The TNF analogue is produced  
 CC recombinantly by E.coli transformed with plasmid pTNF604.  
 CC  
 XX  
 SQ Sequence 151 AA;

Query Match 15.5%; Score 123; DB 12; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 1.6e-05;  
 Matches 46; Conservative 21; Mismatches 66; Indels 28; Gaps 7;

QY 10 DONPOIAHAVISSEASKTTSVLQMAEKGYTMSNNLVTLLENGKQLTVKRGGLYTYAQT 69  
 Db 3 DDKP--VAHV--ANPQAEGLQWLNRRANALLANGVELRD-NQLVVPSSEGLYLYISQVL 57  
 QY 70 F-----CSNFBASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGCGQ 114  
 Db 58 FKGGCGPSTHVLLTHRTISRIASVEQTKVNLISAIKSPCQ-----RETPEGAEAKP-WYE 110  
 QY 115 SIHLGVPFELQPGASVFVNVTDPDSQVSHG--TGFTSFGLLKL 154  
 Db 111 PIYIGVFOLEKGRLSAEINRPDYLDFAESGQVYFGIIAL 151

RESULT 15  
 AAR22311

ID AAR22311 standard; Protein; 150 AA.

XX AAR22311;  
 AC AAR22311;  
 XX  
 DT 04-AUG-1992 (first entry)  
 XX  
 DE TNF polypeptide mutein.  
 XX  
 KM Tumour necrosis factor; anti-tumour; metastasis; cancer; melanoma;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP477791-A.  
 XX  
 PD 01-APR-1992.  
 XX  
 PF 20-SEP-1991; 91EP-0116017.  
 XX  
 PR 17-JUN-1991; 91JP-0240131.  
 PR 21-SEP-1990; 90JP-0250046.  
 XX  
 PA (ISHH ) ISHIBARA SANGYO KAISHA.

XX Yamada N, Kato M, Miyata K, Aoyama Y, Shikama H;  
PI  
XX  
DR WPI, 1992-106202/14.  
XX  
PT New Tumour Necrosis Factor polypeptide mutein - useful in  
PT treating solid tumours e.g. colorectal, lung, gastric and  
PT pancreatic cancers, without promoting tumour metastasis  
XX  
PS Claim 1; Page 35; 55pp; English.  
XX  
CC The protein sequence was obtd. from a synthetic cDNA sequence based  
CC on the human TNF sequence. The synthetic DNA was used to transform E.  
CC coli cells, and the mutein purified by standard chromatography. The  
CC polypeptide is a human TNF N-terminal mutein having anti-tumour  
CC effects similar to those of human TNF but lacking its side effect of  
CC promoting metastasis. It can be used as the active agent in compns.  
CC pref. to treat solid tumours such as colorectal, lung, gastric and  
CC pancreatic cancer, and melanoma and leukaemia.  
CC See also AAR22303-16 and AAR22721-5.  
XX  
SQ Sequence 150 AA;  
SQ  
Query March 15.5%; Score 122.5; DB 13; Length 150;  
Best Local Similarity 28.0%; Pred. No. 1.7e-05;  
Matches 45; Conservative 24; Mismatches 67; Indels 25; Gaps 7;  
QY 8 KGDQNPQIAAHVISEASSKTSVLQMAKGGYYTSMNNLYTLNGKQGLTVKROGLYIYAO 67  
Db 1 RGDKP---VAHV--ANPQAEGLQWLNRANALLANGVELRD--NQLVPSSEGLYLIYSQ 54  
QY 68 VTFCNSREASSQADPFIALSLCKSPGRFERILLRAANTHSSAK-PCGOOS----- 115  
Db 55 VLF----KGQGCPSSTHVLTHRTISRIVASYQTKVNLSSAKSPQORETPEGALAKPYE 109  
QY 116 -IHGAVFEIOPGASVFNVTDPESQVSHG-TGFTSPGLTKL 154  
Db 110 PTYGGVFQLEKGRDLSAEINRPDYLDFAESGVYFGIAL 150

Search completed: June 7, 2003, 12:08:12  
Job time : 71 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2003, 12:05:15 ; Search time 19 Seconds

(without alignments)  
779.195 Million cell updates/sec

Title: US-09-579-548a-1\_COPY\_108\_261

Perfect score: 792  
Sequence: 1 ENSFMQKGDONPQIAAHVI.....TDPQVSHGTGFTSGLTL 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 75564

Minimum DB seq length: 0  
Maximum DB seq length: 154

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	9.2	134	2 H84868	hypothetical prote
2	70.5	8.9	146	2 B70142	ribosomal protei
3	67	8.5	117	2 G97875	hypothetical prote
4	66	8.3	104	2 D95003	hypothetical prote
5	64.5	8.1	138	2 S06571	finger protein (cl
6	64	8.1	133	2 S77897	arginine kinase (E
7	63	8.0	67	2 F81618	hypothetical prote
8	62.5	7.9	126	2 E69201	hypothetical prote
9	61	7.7	137	2 T73213	hypothetical prote
10	60.5	7.6	132	2 F97592	30S ribosomal prote
11	60.5	7.6	132	2 AB2814	hypothetical prote
12	59.5	7.5	146	2 B98347	30S ribosomal prote
13	59.5	7.5	146	2 AE2935	hypothetical prote
14	59	7.4	146	2 A90477	conserved hypot
15	58	7.3	66	2 JN0423	hypothetical prote
16	58	7.3	112	2 A97213	esterase S - fruit
17	57.5	7.3	132	2 F64487	reductase/isomeras
18	57	7.2	123	2 S69460	hypothetical prote
19	57	7.2	147	1 G65063	hypothetical prote
20	57	7.2	147	2 A85933	hypothetical prote
21	57	7.2	147	2 G91087	hypothetical prote
22	56.5	7.1	67	2 T16372	hypothetical prote
23	56.5	7.1	87	1 S18838	A-aggutinin precu
24	56.5	7.1	89	2 C42525	A-ORF-P protein -
25	56.5	7.1	108	1 R3BY31	ribosomal protein
26	56.5	7.1	108	1 S13338	ribosomal protein
27	56.5	7.1	138	2 G82533	50S ribosomal prot
28	56	7.1	149	2 I39768	argd protein - Bac
29	55.5	7.0	127	2 T16131	hypothetical prote

30	55.5	7.0	134	2 G65083	protein glcG - Esc
31	55	6.9	80	2 AH0554	exodeoxyribonuclea
32	55	6.9	128	2 T28438	hypothetical prote
33	55	6.9	129	2 S52792	Ig kappa chain V r
34	55	6.9	134	2 B72651	hypothetical prote
35	55	6.9	139	2 S74816	hypothetical prote
36	55	6.9	144	2 A36335	ribosomal protein
37	55	6.9	152	2 A86557	conserved hypot
38	55	6.9	152	2 F72066	cyat protein - Brw
39	54.5	6.9	106	1 D72700	hypothetical prote
40	54.5	6.9	108	2 D72617	Ig heavy chain - m
41	54.5	6.9	139	2 S18808	ORF2 (bacteriophag
42	54.5	6.9	140	2 AB1653	hypothetical prote
43	54	6.8	117	2 E86230	hypothetical prote
44	54	6.8	125	2 AB2802	hypothetical prote
45	54	6.8	149	2 S13459	hemoglobin - south

## ALIGNMENTS

```
RESULT 1
H84868
hypothetical protein At2g43660 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84868
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84868
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <STO>
A:Cross-references: GB:AE002093; MIM:G2281104; PIDN:AA864040.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g43660
A:Map position: 2

Query Match
Best Local Similarity 26.4%; Score 72.5; DB 2; Length 134;
Matches 32; Conservative 7; Mismatches 25; Indels 57; Gaps 6;

QY 66 AQTFCNSREASSQAPFIAS/CLKSPGRFELRLAANTHS--SAKP-----VTDP 138
Db 4 AQIWF-----PFIILCLISSVGSFMRVNAQAPOGSGWCVAKPPTPIKQIWNLN 53
QY 111 -CGQOSIHL-----GGV-----FELQPGASVFN-----VTDP 138
Db 54 VCSNSVHCEVSBGACYPINLYNSASVYMNLYONQGRQYKCPFGSGIISVDP 113
QY 139 Q 139
Db 114 E 114

RESULT 2
B70142
ribosomal protein L13 (rpL13) - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C:Accession: B70142
R:Fraser, C.M.; Gasjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Keriavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
, Bowman, C.; Giarland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403665
A:Accession: B70142
```

A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-146 <KLE>  
A:Cross-references: GB:AE001140; GB:AE000783; NID:q2688233; PIDN:AA66717.1; PID:g268823  
A:Experimental source: strain B31  
C:Superfamily: Escherichia coli ribosomal protein L13

Query Match 8.9%; Score 70.5; DB 2; Length 146;  
Best Local Similarity 22.8%; Pred. No. 9.2;  
Matches 29; Conservative 21; Mismatches 44; Indels 33; Gaps 6;

QY 16 AAHYSASSTTSTVLQMAEKGYTT---MSNLTLENGK-QLTVK--QGLYIYAQV 68  
DB 27 ADRIKGVADVVKILKSKHAYTTPHODLGDVNIINASKVKLTGKKYQCKLYRRS-- 84  
QY 69 TFCNREASSQAPFIASLCLKSPGRFERILLRANTSSAKPGCGOSIHLCGVLELP-G 127  
DB 85 -----RYPGGLYSDTFR---TLSEKPCAPLEIAIKMLPKGPLG 121  
QY 128 ASVFPNV 134  
DB 122 RNLFRL 128

## RESULT 3

G97875  
Hypothetical protein spr0031 [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C:Accession: G97875  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; Mahren, S.; M  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: G97875  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAK9835.1; PID:g15457561; GSPDB:GN00174  
C:Genetics:  
A:Gene: spr0031

Query Match 8.5%; Score 67; DB 2; Length 117;  
Best Local Similarity 22.0%; Pred. No. 16;  
Matches 26; Conservative 23; Mismatches 43; Indels 26; Gaps 4;

QY 2 NSFEMQGDONPOIAAHVIS---EASSKTTSVLQ-----MAEKGYTMSNNLVT 47  
DB 12 NDLVAKIFSNPEITQFIRDMLDPAKQVTLLEGSDHVLSPYSVDFTSIDVLA 71  
QY 48 LENGKQLTVKROGLYIYAQVTCNREASSQAPFIASLCLKSPGRFERILLRANTH 105  
DB 72 LNDGTVIIEIQ---VHQNPFINH-----LWAVLCSQVNMLEKIHOREGDT 117

## RESULT 4

D95003  
Hypothetical protein SP0031 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C:Accession: D95003  
R:Retzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,  
non, T.; Hickey, E.K.; Holt, I.R.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: D95003  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-104 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AAK74221.1; PID:g14971494; GSPDB:GN00164; TIGR:SF  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0031

Query Match 8.3%; Score 66; DB 2; Length 104;  
Best Local Similarity 22.2%; Pred. No. 17;  
Matches 24; Conservative 22; Mismatches 36; Indels 26; Gaps 4;

QY 12 NPOIAAHVIS---EASSKTTSVLQ-----MAEKGYTMSNNLVTLENGKQLTVK 57  
DB 9 NPEITQFIRDMLDPAKQVTLLEGSDHVLSPYSVDFTSIDVLAELNDGTVIIE 68  
QY 58 RQGLYIYAQVTCNREASSQAPFIASLCLKSPGRFERILLRANTH 105  
DB 69 IQ---VHQNPFINH-----LWAVLCSQVNMLEKIHOREGDT 104

## RESULT 5

S06571  
Finger protein (clone X1CGF4-2) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 10-Oct-1997  
C:Accession: S06571  
R:Nettelbladt, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeling, A.; Kneoc  
J. Mol. Biol. 208, 639-659, 1989  
A>Title: Second-order repeats in Xenopus laevis finger proteins.  
A:Reference number: S06572; MUID:90040698; PMID:2509712  
A:Accession: S06571  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-138 <NIB>  
C:Superfamily: LIM metal-binding repeat homology  
C:Keywords: DNA binding; zinc finger  
F/34-93/Domain: LIM metal-binding repeat homology <LIM4>

Query Match 8.1%; Score 64.5; DB 2; Length 138;  
Best Local Similarity 34.5%; Pred. No. 34;  
Matches 19; Conservative 10; Mismatches 11; Indels 15; Gaps 5;

QY 70 PCSNREASSQ-----APFIASLCLKSPGRF--ERILLR-ANTHSSAKP--CGO 113  
DB 14 PCSNKEIPSKKHITGRPFVCAVC---GKPSDRILLQAHORLHTEKPFCTQ 64

## RESULT 6

S77897  
arginine kinase (EC 2.7.3.3) - Japanese abalone (fragment)  
C:Species: Sulculus diversicolor (Japanese abalone)  
C>Date: 21-Apr-1997 #sequence\_revision 18-Jul-1997 #text\_change 31-Oct-1997  
C:Accession: S77897  
R:Suzuki, T.; Furukohri, T.  
J. Mol. Biol. 237, 353-357, 1994  
A>Title: Evolution of phosphogen kinase. Primary structure of glycocyamine kinase and a  
A:Reference number: S46407; MUID:94194511; PMID:8145248  
A:Accession: S77897  
A:Molecule type: mRNA  
A:Residues: 1-133 <SUZ>  
C:Superfamily: creatine kinase; creatine kinase repeat homology  
C:Keywords: phosphotransferase

Query Match 8.1%; Score 64; DB 2; Length 133;  
Best Local Similarity 21.9%; Pred. No. 37;  
Matches 28; Conservative 20; Mismatches 36; Indels 44; Gaps 5;

QY 6 MOKGQONQOIAAHVISSEASSTTSTVLQMAEKGYTMSNNLVTLENGKQLTVKROGLYIY 65  
DB 6 MOKGDDLAAYVAKRLVMAKMTIASLSLA-----KROGLGYL- 42  
QY 66 AOVTFCSNREASSQAPFIASLCLKSPGR-----FERILLRANTHSSAKPGCGOSI 116

Db	43	---	TFCSNIGTA--	LRASVHKVPRLAQAQPFKEFCDCNHIQAQIH-----	GEHTE	90
Qy	117	HLG	VFEL	124		
		:		:	:	
Db	91	SVGG	VYDL	98		

## RESULT 7

hyponeurical protein CP0063 [imported] - Chlamydomonas pneumoniae (strain AR39)  
C/Species: Chlamydomonas pneumoniae, Chlamydomonas pneumoniae  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000  
C/Accession: F81618  
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.  
A/Reference number: AB1500; MUID:20150255; PMID:10684935  
A/Accession: F81618  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-67 <REA  
A/Cross-references: GB:AE002169; GB:AE002161; NID:g7188991; PIDN:AAF37952.1; PID:g7188999  
C/Experimental source: strain AR39, HL cells  
C/Genetics:  
A/Gene: CP0063

## Query Match

Query Match	8.0%;	Score 63;	DB 2;	length 67;
Best Local Similarity	33.3%;	Score No. 20;		
Matches 19;	Conservative 13;	Mismatches 19;	Indels 6;	Gaps 3;

100 RAANTHSSAKPCGQOSIH LGVFELQPGASVFVNVTDP SQVSHGT--C

Dd  
100 KKAHHSHSNAPCGGSIHLGGVEFLDPGASVFNVTLPSSQVSHGT--GTSFGLIKL 154  
||| | : | : | : | : | : | : | : | :  
12 RAANTIVNKK--QKPFHIGMATLRPNATSLINLIKEDA-LSLGTGVSPASTASIKI 64

## RESULT 8

hypothetical protein MTH6 - *Methanobacterium thermoautotrophicum* (strain Delta H)  
C/Species: *Methanobacterium thermoautotrophicum*  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C/Accession: E69201  
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Otu, D.; Spadafora, R.; Viscare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivanli, N.  
ki, S.; Church, G.M.; Daniels, C.U.; Mao, Y.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: func  
A/Reference number: A69000; MUID:9803514; PMID:9371463  
A/Accession: E69201  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-126 <MTH>  
A/Cross-references: GB:AE000799; GB:AE000666; NID:92621112; PIDN:AMB84582.1; PID:9262111  
A/Experimental source: strain Delta H

## A;Gene: MTH76

Query Match 7.9%; Score 62.5; DB 2; Length 126;  
Best Local Similarity 29.8%; Pred. No. 49;  
Matches 31; Conservative 12; Mismatches 36; Gaps 6

## 22

3' G T I M S N N L V I L E N G K O L I V K R G G L Y I Y A Q V T F C S N R E A S S Q A P I A S L C L K S P O R F E R 96  
 | | : | : | | | : | | : | | |  
 5 G K Y V F A - N L F S V E G V Q R R G K R - - - - C D R N T F C Y A P S R C T S P F S A - - - - - 45

## 27

46 ISLSRVKPNN--KPTSQYONKEAQDISSLQIAAS---NLIPPSQ 84

## RESULT 9

137213  
hypothetical protein Y57G7A.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
C:Accession: 137213

A: Description: The genome of *C. jejuni* 8009 submitted to the EMBL Data Library, March 1999

A:Accession: T37213  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-137 <OZE>  
A:Cross-references: EMBL:AF07542; PIDN:AAC26296.1  
C:Genetics:  
A:Map position: 2  
A:Introns: 34/3; 93/3; 112/3  
A:Note: Y57G7A.1  
C:Superfamily: Caenorhabditis elegans hypothetical protein Y57G7A.1

## Query Match

Query Match	7.7%;	Score 61;	DB 2;	Length 137;
Best Local Similarity	26.5%;	Pred. No. 77;		
Matches 30;	Conservative 17;	Mismatches 46;	Indels 20;	Gaps 6;

Qy

6 MOKGQNPOLAAHVISEASSKTTSTVLQMAEKGYTMSNLTLENGKQLTVKRQ--LYYI 64  
:  
:  
24 LQVDDKDPTLKALVYKEALPRANQKH--DTYYWVP---TTGPSARRITVMNQGLYST 78

Q3

```

QY      65  YAQVTFCSUREASSQAFIASLCLKSPGRFERILLRANATHSSAKPEGQOSIH 117
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DQ      79  WTYDMLGRSDCCSSRSTPLADL-----PG-----CKANTSSPKTLC--SVH 117

```

## RESULT 10

S:50s ribosomal protein S8 (P44249) [imported] - Agrobacterium tumefaciens (strain C58),  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
 C:Accession: F97592  
 R:Goodner, B., Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Leppas, C.; Marwitz, B.  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t  
 A:Reference number: A97559; PMID:11743194  
 A:Accession: F97592  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-132 <KUR>  
 A:Cross-references: GB:AE007869; PID:AAK67655.1; PID:g15157056; GSPDB:GN00169  
 C:Genetics:  
 A:Gene: AGR\_C\_3534  
 A:Map position: circular chromosome  
 C:Superfamily: Escherichia coli ribosomal protein S8

Query Match

Query Match	100%	DB 2	Length 132;	
Best Local Similarity	22.3%;	Pred. No. 82;		
Matches 29; Conservative	14;	Mismatches	36;	Indels 51; Gaps 4

## QY

19 VISEASSKITSLVQMAEKGYITNSNLLVLENGK-QLTVRQGLYIYIAQVTFCSNREAS 77  
 | : ||| | : | ||| : : : || |  
 25 VSTPASLRARVLDVLOSBEGLINGYSKUDPFENGKAEFTIELK--YYEGASY----- 73  
 Db

## QY

```

QY      / 8 SQAPFLASLCCLASPGFRFERILLPANTHSSAKPCGQQSITHLGVEFELQPGASVFVANTDTP 137
      :: || :
Db      74 -----IREIGRVSK-----PGRRVYSVKSI 94

```

## QY

```

qy      138 SQVSHGTGET 147
      ||::|||
Db      95 P0VANGLGIT 104

```

## RESULT 13

AB2814

30S ribosomal protein S8 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)  
 C:Species: *Agrobacterium tumefaciens*  
 C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002  
 C/Accession: AB2814  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
 erage, G.; Gillet, M.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
 A/Reference number: AB2577; PMID:11743193  
 A/Accession: AB2814  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-132 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AAL42928.1; PID:g17740384; GSPDB:GN00186  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: rpsH  
 A:Map position: circular chromosome  
 C:Superfamily: Escherichia coli ribosomal protein S8

Query Match 7.6%; Score 60.5; DB 2; Length 132;  
 Best Local Similarity 22.3%; Pred. No. 82;  
 Matches 29; Conservative 14; Mismatches 36; Indels 51; Gaps 4;  
 Oy 19 VISASSKTTSVLOMAEKGYTMSNNLVTLENGK-QLTVKQGLYYIYAQVTFCSNREAS 77  
 Db 25 VSTRASSIRARVLDVLQSEGYIRGVSKVDPFENGAEFTIELK--YIGASV----- 73  
 Oy 78 SQAFIASLCKSKSGREFRILLRANHTSSAKPCGQOSIHGVELOPGASVFVNVTDP 137  
 Db 74 -----IRETGRVSK-----PGRRVYSVSKSI 94  
 Oy 138 SOVSHGTGFT 147  
 Db 95 PQVANGIGIT 104

RESULT 12  
 B98347  
 hypothetical protein AGR\_L\_3453 [imported] - *Agrobacterium tumefaciens* (strain C58, Cere  
 C:Species: *Agrobacterium tumefaciens*  
 C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 11-Jan-2002  
 C/Accession: B98347  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*  
 A/Reference number: A97359; PMID:11743194  
 A/Accession: B98347  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-146 <KUR>  
 A:Cross-references: GB:AE007870; PIDN:AAK90300.1; PID:g15160327; GSPDB:GN00170  
 C:Genetics:  
 A:Gene: AGR\_L\_3453  
 A:Map position: linear chromosome

Query Match 7.5%; Score 59.5; DB 2; Length 146;  
 Best Local Similarity 32.8%; Pred. No. 1.2e+02;  
 Matches 20; Conservative 4; Mismatches 24; Indels 13; Gaps 2;  
 Oy 93 REFRILLRANHTSSAKPCGQOSIHGVELOPGASVFVNVTDPQVSHGTGFTSPGL 152  
 Db 89 RFRVRFGLA-----GMVGISLAGL---TGA VAVINLTPPSFSFGDNLTAFGNL 135  
 Oy 153 K 153  
 Db 136 Q 136

RESULT 13  
 AE2935  
 conserved hypothetical protein Atu3083 [imported] - *Agrobacterium tumefaciens* (strain C  
 C:Species: *Agrobacterium tumefaciens*  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C/Accession: AE2935  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,  
 erage, G.; Gillet, M.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
 A/Reference number: AB2577; PMID:11743193  
 A/Accession: AE2935  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-146 <KUR>  
 A:Cross-references: GB:AE008689; PIDN:AAL43899.1; PID:g17741448; GSPDB:GN00187  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atu3083  
 A:Map position: linear chromosome

Query Match 7.5%; Score 59.5; DB 2; Length 146;  
 Best Local Similarity 32.8%; Pred. No. 1.2e+02;  
 Matches 20; Conservative 4; Mismatches 24; Indels 13; Gaps 2;  
 Oy 93 REFRILLRANHTSSAKPCGQOSIHGVELOPGASVFVNVTDPQVSHGTGFTSPGL 152  
 Db 89 RFRVRFGLA-----GMVGISLAGL---TGA VAVINLTPPSFSFGDNLTAFGNL 135  
 Oy 153 K 153  
 Db 136 Q 136

RESULT 14  
 A90477  
 hypothetical protein SSO2967 [imported] - *Sulfolobus solfataricus*  
 C:Species: *Sulfolobus solfataricus*  
 C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C/Accession: A90477  
 R:She, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char  
 Jung, I.; Jeffries, A.C.; Kozers, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,  
 submitted to GenBank, April 2001  
 A>Description: *Sulfolobus solfataricus* complete genome.  
 A/Reference number: A99139  
 A/Accession: A90477  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-146 <KUR>  
 A:Cross-references: GB:AE006641; NID:g13816347; PIDN:AAK43072.1; GSPDB:GN00155  
 C:Genetics:  
 A:Gene: SSO2967

Query Match 7.4%; Score 59; DB 2; Length 146;  
 Best Local Similarity 25.0%; Pred. No. 1.3e+02;  
 Matches 22; Conservative 16; Mismatches 36; Indels 14; Gaps 4;  
 Oy 12 NPOIAHVISAASSKTTSVLOMAEKGYTMSNNLVTLENGKQLTVKQGLYYIYAQVTFPC 71  
 Db 30 NPFISSAVSRRLGGS-----MSVQNTYS-GNNVT-----EILIDQGNLVITQYSFP 78  
 Oy 72 SNREASSQAPPIALCLCKSPRFRILL 99  
 Db 79 SVTQKQS---FFYANSLGQVEYENYLI 103

RESULT 15  
 JN0423  
 esterase S - fruit fly (*Drosophila virilis*) (fragment)





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OM protein - protein search, using sw model

Run on: June 7, 2003, 12:04:41 ; Search time 10 Seconds  
(without alignments)  
638.735 Million cell updates/sec

Title: US-09-579-548a-1\_COPY\_108\_261  
Perfect score: 792

Sequence: 1 ENSFMQKGDNPQIAAHVT.....TDPQVSHGTGFTSGLLKL 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 26877

Minimum DB seq length: 0  
Maximum DB seq length: 154

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	111	14.0	150	1	TNFC_PIG
2	70.5	8.9	146	1	Q9TSV8 sus scrofa
3	64.5	8.1	138	1	RI13_BORBU
4	64	8.1	130	1	ZG44_XENLA
5	57.5	7.3	132	1	MSRB_PASNU
6	57	7.2	147	1	YF03_METUA
7	56.5	7.1	87	1	YGDK_ECOLI
8	56.5	7.1	89	1	AGAD2_YEAST
9	56.5	7.1	108	1	YVAP_YACCC
10	56	7.1	149	1	RS25_YEAST
11	55.5	7.0	134	1	ARGD_BACST
12	55	6.9	134	1	GLCG_ECOLI
13	55	6.9	134	1	SPH1_AERPE
14	55	6.9	134	1	RS14_TRYRB
15	54.5	6.9	152	1	Y333_CHLUP
16	54	6.8	106	1	Y333_CHLUP
17	54	6.8	149	1	GLB2_MORMR
18	53.5	6.8	151	1	HPB1_CASGL
19	53.5	6.8	116	1	RS16_CHLMU
20	53.5	6.8	129	1	Y804_HAEIN
21	53	6.7	152	1	Y804_HAEIN
22	53	6.7	152	1	Y804_HAEIN
23	52.5	6.6	80	1	Y804_HAEIN
24	52.5	6.6	110	1	Y804_HAEIN
25	52.5	6.6	130	1	Y804_HAEIN
26	52.5	6.6	132	1	Y804_HAEIN
27	52.5	6.6	150	1	Y804_HAEIN
28	52	6.6	79	1	Y804_HAEIN
29	52	6.6	116	1	Y804_HAEIN
30	52	6.6	153	1	Y804_HAEIN
31	51.5	6.5	75	1	Y804_HAEIN
32	51.5	6.5	108	1	Y804_HAEIN
33	51.5	6.5	125	1	Y804_HAEIN

34	51.5	6.5	128	1	Y804_YEAST	P40057 saccharomyc
35	51	6.4	92	1	PPIC_SALTY	Q91663 salmonella
36	51	6.4	116	1	RS17_PYRAB	Q91663 pyrococcus
37	51	6.4	116	1	RS17_PYRAB	Q91663 pyrococcus
38	51	6.4	150	1	Y802_SCHPO	Q10081 schizosacch
39	51	6.4	151	1	HBPA_CASGL	Q42665 casuarina g
40	50.5	6.4	91	1	RR19_SOYBN	Q07816 glycine max
41	50.5	6.4	105	1	API_BOVIN	Q07816 bos taurus
42	50.5	6.4	111	1	SOH4_ECOLI	P15373 escherichia
43	50.5	6.4	146	1	DUT_ZYMO	Q93345 zymomonas m
44	50.5	6.4	149	1	MOAE_ECOLI	P30749 escherichia
45	50	6.3	93	1	SY14_HUMAN	Q16627 homo sapien

## ALIGNMENTS

```

RESULT 1
TNFC_PIG
AC Q9TSV8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE necrosis factor ligand superfamily member 3) (Fragment).
GN LTB OR TNFRSF3 OR TNFC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Fibroblast;
RX MEDLINE=21108615; PubMed=11169259;
RA Chardon P., Rogel-Gallard C., Catolico L., Duprat S., Vaiman M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes.";
RL Tissue Antigens 57:55-65(2001).
CC -!- FUNCTION: Cytokine that binds to LTB/R/TNFRSF3. May play a specific
CC role in immune response regulation. Provides the membrane anchor
CC for the attachment of the heterotrimeric complex to the cell
CC surface.
CC -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC (less prevalent) two LTA and one LTB subunits.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL: AJ251914; CAB63851.1; -
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF_1
CC PRINTS: PR01234; TNFCROSISFCT.
CC ProDom: PD002012; TNF_abc; 1.
CC SMART: SMO0207; TNF_1.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS0049; TNF_2; 1.
CC Cytokine; Cytotoxin; Glycoprotein.
CC NON_TER
CC CARBOHYD
FT 128 128 N-LINKED (GLCNAC... ) (POTENTIAL)
SO SEQUENCE 150 AA; 16423 MW; F55C4CC657658B48 CRC64;
Query Match 14.0%; Score 111; DB 1; Length 150;
Best Local Similarity 25.9%; Pred. No. 0.00016;

```

Matches 36; Conservative 16; Mismatches 67; Indels 20; Gaps 3;

QY 31 LOWAEKYYIMSNLVLTLENGKQLTVMKQGLYYIAQVTFCSNREASSAPFLASLCKS 90  
 DB 8 LGWEAKKEAEFLRGSTPGSAEGALPDGGLYYLCHVGRAPPPGDDPLDRSVTLIS 67  
 QY 91 -----PGRFERILLRAANT-----HSSAPCCQGSIHGVELEPGASVVF 131  
 DB 68 RLVRAGAGAYGGTPE-LLBGAETVTPVLDPSRHEVGPLMYTISVGGLVQLRRGERV 126  
 QY 132 VNVTDPSCVSHGTGFTSFG 150  
 DB 127 VNISHPMVDYRRGKTFFG 145

## RESULT 2

RL13\_BORBU STANDARD; PRT; 146 AA.  
 AC 051314;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein L13.  
 GN RPLM OR BB0339.  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.  
 NC NCB1\_TaxID=139;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35210 / B31;  
 RX MEDLINE=98065943; PubMed=9403685;  
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,  
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,  
 RA Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,  
 RA Peterson J., Karpavage A.R., Quackenbush J., Salzberg S., Hanson M.,  
 RA van Vugt R., Palmer M.D., Adams M.D., Gocayne J.D., Weidman J.,  
 RA Uitterlind T., Matthey L., McDonald L., Artach P., Bowman C.,  
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,  
 RA Smith H.O., Venter J.C.;  
 RT \*Genomic sequence of a Lyme disease spirochete, Borrelia  
 RT burgdorferi.\*  
 RL Nature 390:580-586(1997).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE EARLY ASSEMBLY PROTEINS OF  
 CC THE 50S RIBOSOMAL SUBUNIT (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL: AE001140; AAC66717.1; -.  
 CC DR TIGR: BB0339; -.  
 DR InterPro: IPR001074; Ribosomal L13.  
 DR Pfam: PF00572; Ribosomal\_L13.1.  
 DR ProDom: PD001791; Ribosomal\_L13.1.  
 DR TIGRFAMs: TIGR01066; rplM\_bact; 1.  
 DR PROSITE: PS00783; RIBOSOMAL\_L13; 1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 146 AA; 16694 MW; 62C15E28A6B45C2F CRC64;

Query Match 8.9%; Score 70.5; DB 1; Length 146;  
 Best Local Similarity 22.8%; Pred. No. 2.6;  
 Matches 29; Conservative 21; Mismatches 44; Indels 33; Gaps 6;

QY 16 AAHVISEASSTKTVLOWAEKYYT-----MSNNLVLTLENGK-QLTYKR--QGLYYIYAGV 68  
 DB 27 ADRIIGKAVVDVVKILRGKHAYTTHQDLGDNVILINASKYVLTKKQOQKLYTHS-- 84  
 QY 69 TFCNSREASSQAPFLASLCKSPGRFERILLRAANTHSSAKPCQGSIHGVELEPG- 127

DB 85 -----RYPGALYSDFTR-----TLSEKRCAPLEIAIKMLPKGPLG 121  
 QY 128 ASVFPNV 134  
 DB 122 RNLFRLN 128

## RESULT 3

ZG44\_XENLA STANDARD; PRT; 138 AA.  
 ID ZG44\_XENLA  
 AC P18721;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Gastrula zinc finger protein XLGF44.2 (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NC NCB1\_TaxID=8355;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=90040698; PubMed=2509712;  
 RA Metteld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,  
 RA Poetling A., Knoechel W.;  
 RT "Second-order repeats in Xenopus laevis finger proteins.";  
 RL J. Mol. Biol. 208:639-659(1989).  
 DR PIR: S06571; S06571.  
 DR InterPro: IPR000822; Znf\_C2H2.  
 DR Pfam: PF00096; Zf\_C2H2\_5.  
 DR SMART: SM00355; Znf\_C2H2; 5.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 5.  
 DR PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 5.  
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 5 27 C2H2-TYPE.  
 FT ZN\_FING 32 54 C2H2-TYPE.  
 FT ZN\_FING 60 82 C2H2-TYPE.  
 FT ZN\_FING 88 110 C2H2-TYPE.  
 FT ZN\_FING 116 138 C2H2-TYPE.  
 FT NON\_TER 138 138  
 SQ SEQUENCE 138 AA; 16316 MW; 3FC025908EEF43AB CRC64;

Query Match 8.1%; Score 64.5; DB 1; Length 138;  
 Best Local Similarity 34.5%; Pred. No. 10;  
 Matches 19; Conservative 10; Mismatches 11; Indels 15; Gaps 5;

QY 70 FCSNRASSO-----APTASLCKSPGRF-ERILRA-ANTHSSAKP-CGQ 113  
 DB 14 FCSNKELFSHKRIHTGRPPVCAVC-----GKYFSDRIILQAHQRLTGRKPTCTQ 64

## RESULT 4

MSRB\_PASMU STANDARD; PRT; 130 AA.  
 ID MSRB\_PASMU  
 AC Q9CMB1;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptide methionine sulfoxide reductase msrb (EC 1.8.4.6).  
 GN MSRB OR PM0923.  
 OS Pasteurella multocida.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Pasteurella.  
 NC NCB1\_TaxID=747;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Pm70;  
 RX MEDLINE=21145866; PubMed=11248100;  
 RA May B.Y., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;  
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

```
CC      -1- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin =
CC      protein L-methionine S-oxide + reduced thioredoxin.
CC      -1- SIMILARITY: BELONGS TO THE MSRB MET SULFOXIDE REDUCTASE FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; A600631; AAK03007.1; -
DR      InterPro; IPR000345; CytC_heme_bind.
DR      InterPro; IPR002579; DUF25.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF01641; DUF25; 1.
DR      ProDom; PD004057; DUF25; 1.
DR      TIGRfam; TIGR00357; DUF25; 1.
DR      Oxidoreductase; Complete proteome.
KM      ACT_SITE 111 111
PT      ACT_SITE 111 111
SQ      SEQUENCE 130 AA; 14675 MW; CC5975080A564A95 CRC64;
CC      -----
Query Match
Best Local Similarity 29.8%; Score 64; DB 1; Length 130;
Matches 25; Conservative 12; Mismatches 33; Indels 14; Gaps 4;
CC      -----
Qy      51 GKQLTWRKQGLYYIAOVAFCNREASQAPFASLCLKSPGRFHI---LLEAANTHS 107
Db      26 GKLDLQOKKGLY-----RCVCHSPLEFVSPTKFDAG--CCMPSPFOAISPEAIRYLDYTL 79
Qy      108 AKP-----CGGQSHHGVEFLQIP 126
Db      80 SRPRTETRCQGDALHGHVFEDGP 103
CC      -----
RESULT 5
YF03_METUA
ID      YF03_METUA STANDARD; PRT; 132 AA.
AC      Q58898;
DC      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein M01503.
GN      M01503.
OS      Methanococcus jannaschii.
OC      Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC      Methanocaldococcaceae; Methanocaldococcus.
OX      NCBI_TaxID=2190;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX      MEDLINE=96337999; PubMed=6688087;
RA      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA      Sutton G.G., Blake J.A., FitzGerald J.M., Clayton R.A., Gocayne J.D.,
RA      Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Gilecki A.,
RA      Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA      Utechtack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA      Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA      Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA      "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT      jannaschii."
RL      Science 273:1056-1073(1996).
CC      -----
-1- SIMILARITY: STRONG, TO M JANNASCHII M01082.
CC      -----
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CC      -----
DR      EMBL; U67591; AAB99516.1; -.
DR      TIGR; M01503; -.
KM      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 132 AA; 15528 MW; 44046F77C6F1D0CD CRC64;
CC      -----
Query Match
Best Local Similarity 22.8%; Score 57.5; DB 1; Length 132;
Matches 13; Conservative 11; Mismatches 28; Indels 5; Gaps 1;
CC      -----
Qy      19 VISEASKTTVYLQMAEKGYTMSNNLVLENG-----KQTVRQGLYYIAQVTF 70
Db      36 ILKNGPSKINDIAERINRDRSTVQRAVQNLNMGVLRKQVNIKGGYIVYEAIP 92
CC      -----
RESULT 6
YGDK_ECOLI
ID      YGDK_ECOLI STANDARD; PRT; 147 AA.
AC      Q46926;
DC      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein YgdK.
GN      YGDK OR B2811 OR Z4128 OR ECS3671.
OS      Escherichia coli, and
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
OX      NCBI_TaxID=562, 83334;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12 / MG1655;
RX      MEDLINE=9742617; PubMed=9278503;
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.;
RT      "The complete genome sequence of Escherichia coli K-12."
RL      Science 277:1453-1474(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX      MEDLINE=21074935; PubMed=11206551;
RA      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA      Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA      Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA      Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA      Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA      Welch R.A., Blattner F.R.;
RT      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL      Nature 409:529-533(2001).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / RIMD 0509952;
RX      MEDLINE=21156231; PubMed=11258796;
RA      Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA      Han C.-G., Ohtsuno E., Nakayama K., Muraoka T., Tanaka M., Tobe T.,
RA      Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA      Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT      "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT      O157:H7 and genomic comparison with a laboratory strain K-12."
RL      DNA Res. 8:11-22(2001).
CC      -----
-1- SIMILARITY: BELONGS TO THE UFP0050 FAMILY.
CC      -----
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ID RS25 YEAST STANDARD; PRT; 108 AA.  
AC P07282; P05758;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 40S ribosomal protein S25 precursor (S21) (RS23) (RP45)  
GN (RPS25A OR RPS31A OR YGR027C) AND (RPS25B OR RPS31B OR RPS31 OR YLR33C OR L8100.10).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OK NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Carlsbergensis;  
RX MEDLINE=91091952; PubMed=2856436;  
RA Nieuwint R.T.M., Molenaar C.M.T., van Bommel J.H.,  
RA van Raamsdonk-Duin M.M.C., Mager W.H., Planta R.J.,  
RT "The gene for yeast ribosomal protein S31 contains an intron in the  
RT leader sequence."  
RL Curr. Genet. 10:1-5(1985).  
RL [2]  
RP SEQUENCE FROM N.A. (RPS25B).  
RC STRAIN=S288c / AB972;  
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J.,  
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,  
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,  
RA Mardis E., Meneses S., Miller N., Nhan N., Pauley A., Peluso D.,  
RA Rifken L., Riles L., Tatch A., Trevasakis E., Vignati D.,  
RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston D.,  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (RPS25A).  
RC STRAIN=S288c;  
RX MEDLINE=97435481; PubMed=9250212;  
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.,  
RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae  
RT chromosome VII."  
RL Yeast 13:1077-1090(1997).  
RN [4]  
RP SEQUENCE OF 15-22.  
RA Otake E., Higo K.-I., Itoh T.,  
RT "Yeast ribosomal proteins: VII. Isolation of two proteins and  
RT sequence characterization of twenty-four proteins from cytoplasmic  
RL ribosomes."  
RL Mol. Gen. Genet. 195:544-546(1984).  
CC -!- MISCELLANEOUS: IT IS PRESUMED THAT THE PRECURSOR PART OF S25 IS  
CC ENGAGED IN ASSEMBLING OF THE SMALL SUBUNIT, THUS BEING ESSENTIAL  
CC IN RIBOSOME MATURATION.  
CC -!- SIMILARITY: BELONGS TO THE S25E FAMILY OF RIBOSOMAL PROTEINS.  
CC  
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CC  
DR EMBL: X03013; CA26797.1; -  
DR EMBL: U19028; AAB67260.1; -  
DR EMBL: Z72812; CAA97010.1; -  
DR PIR: S05844; R3BY31.  
DR SCD: S0003259; RPS25A.  
DR SCD: S0004325; RPS25B.  
DR InterPro: IPR004977; Ribosomal\_S25.  
DR Pfam: PF03297; Ribosomal\_S25.  
KM Ribosomal protein, Multigene family.  
FT PROPEP 1 14  
FT CHAIN 15 108  
FT VARIANT 105 105 A -> T (IN RPS25A).

FT CONFLICT 16 16 A -> R (IN REF. 4).  
SQ SEQUENCE 108 AA; 12009 MW; C52D0334EAI25B5 CRC64;  
Query Match  
Best Local Similarity 7.1%; Score 56.5; DB 1; Length 108;  
Matches 22; Conservative 14; Mismatches 51; Indels 13; Gaps 1;  
OY 16 AAHVISEASSKTSVLTQMAEGYVTMSNIVTLKNGKQIVTKRGGLYITIAQVTCNRE 75  
DB 10 AAKAALAGKSKSKKSKSKMDRQAHVILDOEKYDRLKEVPTRYVSVLVDR- 68  
OY 76 ASSQAPFIASLCIKSPERFIRILLRANTSSAKPCQGS 115  
DB 69 -----LKIGGSILRIALRHLKEGIIKPSKIS 96  
RESULT 10  
ARGD\_BACST  
ID ARGD\_BACST STANDARD; PRT; 149 AA.  
AC C07907;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Acetylornithine aminotransferase (EC 2.6.1.11) (ACOAT) (Fragment).  
GN Bacillus stearothermophilus.  
OS Bacillus stearothermophilus.  
OC Bacteria; Firmicutes; Bacillales; Geobacillus.  
OK NCBI\_TaxID=1422;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCIB 8224;  
RX MEDLINE=93232760; PubMed=8473852;  
RA Sakanyan V., Charlier D.R.M., Legrain C., Kochikyan A., Mett I.,  
RA Pierard P., Glansdorff N.,  
RT "Primary structure, partial purification and regulation of key  
RT enzymes of the acetyl cycle of arginine biosynthesis in Bacillus  
RT stearothermophilus: dual function of ornithine acetyltransferase."  
RL J. Gen. Microbiol. 139:393-402(1993).  
CC -!- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + 2-oxoglutarate = N-  
CC acetyl-L-glutamate 5-semialdehyde + L-glutamate.  
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -!- PATHWAY: Arginine biosynthesis; fourth step.  
CC -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL- PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
CC  
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CC  
DR EMBL: U06036; AAA22199.1; -  
DR HSSP: P12995; I0J5.  
DR InterPro: IPR000954; Aminotran\_3.  
DR Pfam: PF00202; aminotran\_3.1.  
DR PROSITE: PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
KM Transferase; Aminotransferase; Pyridoxal phosphate;  
KM Arginine biosynthesis.  
FT NON\_TER 149 149  
SQ SEQUENCE 149 AA; 16541 MW; 1A1FA96510D34D6F CRC64;  
Query Match  
Best Local Similarity 7.1%; Score 56; DB 1; Length 149;  
Matches 22; Conservative 15; Mismatches 38; Indels 12; Gaps 4;  
OY 39 YTMNSNLTLL---ENGKQLTVKRGGLYIYAQVTCNREASSQAPFIASLCIKSPGRPE 95  
DB 61 YMHVSNLFTPIQDEAVASLVVHSAQDYV-----FCNSGAENNEAL--KLARKTGRHK 114  
OY 96 RILUPAA---NTHSSAKPCQGSIHG 119

Db 115 VITROSFGHRTFATMAATGOKVHSG 141

```

RESULT 11
GLCG ECOLI
ID GLCG ECOLI STANDARD; PRT; 134 AA.
AC P45504;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein glcG
GN GLCG OR B2977.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RA MEDLINE=96178972; PubMed=8606183;
RA Pellicer M.T., Badia J., Aguilar J.T., Baldoma L.;
RT "glc locus of Escherichia coli: characterization of genes encoding
RL the subunits of glycolate oxidase and the glc regulator protein.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGL655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kittpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Siao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE OF 59-134 FROM N.A.
RC STRAIN=K12 / W3110;
RA MEDLINE=95010032; PubMed=7925370;
RA Molina I., Badia J., Aguilar J.T., Pellicer M.T., Baldoma L.;
RT "Molecular characterization of Escherichia coli malate synthase G.
RL Differentiation with the malate synthase A isoenzyme.";
CC -1- SIMILARITY: TO C. FREUNDII HYPOTHETICAL PROTEIN IN DHAT-DHAS
CC INTERGENIC REGION (ORF) (AC P4517).
CC -----
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CC -----
DR EMBL; LA3490; AAB02533.1; -
DR EMBL; U28377; AAA69144.1; -
DR EMBL; AE000380; AAC76013.1; -
DR EMBL; X74547; -; NOT ANNOTATED_CDS.
DR EcoGene; E02952; glcG.
DR Complete proteome.
FT CONFLICT 128 134
FT SEQUENCE 134 AA; 13737 MW; 43DBA615A6E60A6A CRC64;
SQ
Query Match 7.0%; Score 55.5; DB 1; Length 134;
Best Local Similarity 29.7%; Pred. No. 86;
Matches 19; Conservative 11; Mismatches 23; Indels 11; Gaps 2;
QY 6 MOKGDPQIAAHVISEASSTTSLVOMAEKGYTWSNN-----LVTLLENKQJLT 55
Db 44 LSRMPDCAPAIAY-ISOEKAFATAGRETKYEEMVNNKRTAFATPALTSLBEGVPV 102
QY 56 VKRQ 59
Db 103 VDGQ 106

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RESULT 12
SPH1_AERPE
ID SPH1_AERPE STANDARD; PRT; 134 AA.
AC Q9YED6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme 1 (EC 4.1.1.50) (AdoMetDC
DE 1) (SambD 1) [Contains: S-adenosylmethionine decarboxylase 1 beta
DE chain; S-adenosylmethionine decarboxylase 1 alpha chain].
GN SPH1 OR APE0639.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:81-101(1999).
CC -1- FUNCTION: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
CC AMINO-PROPYL MOIETY REQUIRED FOR SPERMIDINE BIOSYNTHESIS FROM
CC PUTRESCINE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-
CC adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC ADOMETDC FAMILY. SUBFAMILY
CC 1.
CC -----
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CC -----
DR EMBL; AP000060; BAA79610.1; -
DR InterPro; IPR003826; SAMDC.
DR Pfam; PF02675; DUF206; 1.
KW Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
KW Complete proteome.
FT CHAIN 1 81
FT FT
FT CHAIN 82 134
FT FT
FT SITE 81 82
FT MOD_RES 82 82
FT FT
FT SEQUENCE 134 AA; 14845 MW; 57942011P9A404C4 CRC64;
SQ
Query Match 6.9%; Score 55; DB 1; Length 134;
Best Local Similarity 30.2%; Pred. No. 97;
Matches 16; Conservative 8; Mismatches 17; Indels 12; Gaps 2;
QY 50 NGKULTVRQGLLYIYAQVTFCSNREASQAFIASLCKSPGFPERILRAA 102
Db 14 NGSGAQMRVFL-HVYGNFYECANTE-----LMSPELEKVVLEDA 54
QY
Db
RESULT 13
RS14_TRYBB
ID RS14_TRYBB STANDARD; PRT; 144 AA.

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AC P19800;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DR 40S ribosomal protein S14.
GN RPS14.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RX MEDLINE=90258927; PubMed=2188114;
RA Pereleman D., Boothroyd J.C.;
RL Mol. Cell. Biol. 10:3284-3288(1990).
CC -1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
CC EMBL; M36124; AAA30237.1; -
CC PIR; A36335; A36335.
CC InterPro: IPR001971; Ribosomal_S11.
CC Pfam; PF00411; Ribosomal_S11; 1.
CC ProDom; PD001010; Ribosomal_S11; 1.
CC PROSITE; PS00054; RIBOSOMAL_S11; 1.
CC Ribosomal protein.
CC SEQUENCE 144 AA; 15513 MW; 1055963B279F799 CRC64;

Query Match 6.9%; Score 55; DB 1; Length 144;
Best Local Similarity 24.0%; Pred. No. 1.1e+02;
Matches 29; Conservative 14; Mismatches 26; Indels 52; Gaps 7;

QY 35 EKGYYTSMNVLVTLENGKQLVVKQGLYIYA-----QVTF----- 71
DB 6 EVKTYGSS-----AGKQQLV--YGVVHIYASFNDFVHTVDSMGRFCKVTCGMKVK 56
QY 72 SNREASSQAPFIASLCTKSPGRFERILLRAANTHSSAKPCGQOSIH-----GGVFELDP 126
DB 57 ADDRESS--PYVA-----MMAADVVYARCKECGINALHVMRATGVGVTKSP 101
QY 127 G 127
DB 102 G 102

RESULT 14
Y533_CHLPN STANDARD; PRT; 152 AA.
AC Q92819;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CP0219/CPJ0533.
GN CPN0533 OR CP0219 OR CPJ0533.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kaiman S., Mitchell W., Marathe R., Lamme C., Fan J., Hyman R.W.,
RA Olinger U., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).

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RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39."
RT Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- SIMILARITY: BELONGS TO THE UPF0168 FAMILY.
CC -----
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CC -----
CC EMBL; AE001638; AAD18673.1; -
CC DR; AE002183; AA38088.1; -
CC DR; EMBL; AF002547; BAA98739.1; -
CC DR; TIGR; CP0219; -
CC InterPro: IPR005144; ATP.
CC InterPro: IPR003796; DUF193.
CC Pfam; PF03477; ATP-cone; 1.
CC TIGRFAMs; TIGR00244; TIGR00244; 1.
CC Hypothetical protein; Complete proteome.
CC SEQUENCE 152 AA; 17467 MW; FDA90454037B7750 CRC64;

Query Match 6.9%; Score 55; DB 1; Length 152;
Best Local Similarity 29.4%; Pred. No. 1.1e+02;
Matches 15; Conservative 6; Mismatches 26; Indels 4; Gaps 1;

QY 71 CSNREASSQAPFIASLCTKSPGRFERI---LRAANTHSSAKPCGQOSIH 117
DB 34 CSQRTFTFVELTLOVLRKDGKRYENQESKLIHGLNAASSHRTIGODVN 84

RESULT 15
CYAY_ERWCH
ID CYAY_ERWCH STANDARD; PRT; 106 AA.
AC P40128;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyay protein.
GN CYAY.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B374;
RX MEDLINE=89055613; PubMed=3057176;
RA Danchin A., Lenz G.;
RT "Structure and evolution of bacterial adenylate cyclase: comparison
RT between Escherichia coli and Erwinia chrysanthemi.";
RL Second Messengers Phosphoproteins 12:7-26(1988).
CC -1- SIMILARITY: BELONGS TO THE FRATAXIN FAMILY.

```



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DR EMBL; X63207; CAA44892.1; -;  
DR HSSP; P27838; IEW4.  
DR InterPro; IPR002908; Frataxin\_1ike.  
DR Pfam; PF01491; Frataxin\_Cyay; 1.  
DR ProDom; PD006646; Frataxin\_1ike; 1.  
DR PROSITE; PS01344; FRATAXIN\_1; 1.  
DR PROSITE; PS50810; FRATAXIN\_2; 1.  
SQ SEQUENCE 106 AA; 12036 MW; 66EBE25CB1267AE4 CRC64;

Query Match  
Best Local Similarity 6.9%; Score 54.5; DB 1; Length 106;  
Matches 15; Conservative 12; Mismatches 27; Indels 15; Gaps 2;

Qy	39	YTMNNLVTL--ENGKLTVRQ-----	GLYIYAQVTFCNREASSQAPPI	83
Db	32	YETNGVMTLSFENGSKIIVINRQEPHGVWLTAKGGYHFDYQHGKRWICDRSGSDPMAL	:	91
Qy	84	ASLCLKSPG 92		
Db	92	AQACTEOSG 100		

Search completed: June 7, 2003, 12:06:56  
Job time : 12 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2003, 12:04:41 ; Search time 78 Seconds  
(without alignments)  
406.811 Million cell updates/sec

Title: US-09-579-548A-1\_COPY\_108\_261  
Perfect score: 792  
Sequence: 1 ENSFEMOKGQNPQIAAHV.....TDEPSQVSHGTGFTSFGILKL 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 223313

Minimum DB seq length: 0  
Maximum DB seq length: 154

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: SP archaea:\*
  - 2: SP bacteria:\*
  - 3: SP fungi:\*
  - 4: SP human:\*
  - 5: SP invertebrate:\*
  - 6: SP mammal:\*
  - 7: SP mhc:\*
  - 8: SP organelle:\*
  - 9: SP phage:\*
  - 10: SP plant:\*
  - 11: SP rodent:\*
  - 12: SP virus:\*
  - 13: SP vertebrate:\*
  - 14: SP unclassified:\*
  - 15: SP virus:\*
  - 16: SP bacteriopl:\*
  - 17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	15.4	149	6	097538
2	122	15.4	149	6	097538
3	120.5	15.2	138	6	097538
4	118	14.9	149	6	097538
5	73.5	9.3	99	6	095158
6	72.5	9.2	134	10	022837
7	72.5	9.0	93	6	097538
8	68.5	8.6	111	16	09CJN4
9	66	8.3	104	16	097538
10	65.5	8.3	140	2	09ZSN4
11	65.5	8.3	101	11	09R136
12	64.5	8.1	104	6	027978
13	64	8.1	88	13	090WP9
14	64	8.1	140	2	09S3B6
15	63	8.0	67	16	09K2E4
16	63	8.0	140	2	09S3D4

17	63	8.0	140	2	09S3D2	09s3d2 helicobacte
18	62.5	7.9	126	17	026180	026180 methanobacte
19	62.5	7.9	140	2	08V1B9	08v1b9 helicobacte
20	62	7.8	140	2	09S3E8	09s3e8 helicobacte
21	61.5	7.8	141	17	08ZWK8	08zwk8 pyrobaculum
22	61	7.7	137	5	076628	076628 caenothabdi
23	61	7.7	140	2	09S3E4	09s3e4 helicobacte
24	61	7.7	140	2	09S3D7	09s3d7 helicobacte
25	61	7.7	140	2	09S3D6	09s3d6 helicobacte
26	61	7.7	140	2	09S3D5	09s3d5 helicobacte
27	61	7.7	140	2	09S3E5	09s3e5 helicobacte
28	61	7.7	140	2	08VNH1	08vnh1 helicobacte
29	61	7.7	140	2	08VNH0	08vnh0 helicobacte
30	60.5	7.6	121	9	08SCT3	08sct3 pseudomonas
31	60.5	7.6	124	16	08RAW1	08raw1 thermoaer
32	60.5	7.6	132	16	08UB32	08ub32 agrobacteri
33	60	7.6	140	2	09S3D9	09s3d9 helicobacte
34	60	7.6	140	2	09S3D3	09s3d3 helicobacte
35	60	7.6	140	2	08VNI9	08vni9 helicobacte
36	60	7.6	140	2	08VNH6	08vnh6 helicobacte
37	60	7.6	140	2	08VNH2	08vnh2 helicobacte
38	60	7.6	140	2	08VLI9	08vli9 helicobacte
39	59.5	7.5	115	4	08TCB4	08tcb4 homo sapien
40	59.5	7.5	146	16	08UBD3	08ubd3 agrobacteri
41	59.5	7.5	147	2	09FE63	09fe63 streptococc
42	59	7.4	126	4	09S545	09s545 homo sapien
43	59	7.4	130	2	09XDA8	09xda8 mycobacteri
44	59	7.4	140	2	08VNH4	08vnh4 helicobacte
45	59	7.4	140	2	08VNG8	08vng8 helicobacte

ALIGNMENTS

RESULT 1

ID 097538 PRELIMINARY; PRT; 149 AA.

AC 097538;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)

DE Tumor necrosis factor alpha (Fragment).

GN TNF-ALPHA.

OS Aotus vociferans (noisy night monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

NCBI\_TaxID=57176;

RN [1]

RP SEQUENCE FROM N. A.

RA Echeverry S.J., Hernandez E., Moreno A., Patarro M.E., Murillo L.A.;

RT "Identification, cloning and sequencing of different interleukin genes

RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF014508; AAD01534.1; -

DR HSSP; P01375; ATSV

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR00478; TNF\_Family.

DR Pfam; PF00229; TNF\_1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF\_1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS0049; TNF\_2; 1.

FT NON\_TER

FT NON\_TER

FT SEQUENCE

SO 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query March 15.4%; Score 122; DB 6; Length 149;

Best Local Similarity 30.1%; Pred. No. 6.7e-05;

Matches 46; Conservative 23; Mismatches 56; Indels 28; Gaps 7;

17 AHVISEASRTTSLVQWAEKGYVTMSNNLVTLFENGKQITVXRQGLTYIYQVTF-----70

Db 7 AHV--ANPQAEQOLWLNRRANALLANGVELRD-NQLVVPSEGLVYVSQVLFKQGGCP 63  
QY 71 -----CSNREASSQAPFIASLCLKSPGRFERILLRANTHSSAKPCQGSIHLCGV 121  
Db 64 STEMLLTHSISRIASVQAKVNLISAIKSP--CORETPRKAATNPMYEP-----IYLGV 116  
QY 122 FELQPG--ASVFNVTDPQSVSHGTGTSFGLL 152  
Db 117 FOLEKGDRLSAEINLPDYLDLAR-SQVYFGLI 148

## RESULT 2

Q9TTG8 PRELIMINARY; PRT; 149 AA.  
AC Q9TTG8;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Tumor necrosis factor alpha (Fragment).  
GN TNF-ALPHA.  
OS Aotus nigriceps (black-headed night monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
OX NCBI\_TaxID=57175;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,  
RA Patario M.E.;  
RT "Aotus nigriceps gene for TNF alpha";  
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF097328; AAF21303.1; -.  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR00478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SMO0207; TNF\_1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCD1E689 CRC64;

Query Match 15.4%; Score 122; DB 6; Length 149;  
Best Local Similarity 30.1%; Pred. No. 6.7e-05;  
Matches 46; Conservative 23; Mismatches 56; Indels 28; Gaps 7;

QY 17 AHVSEASSKTTSTVLQMAEKGYTMSNNLVTLENGKQLTVKROGLYYIAQVTF----- 70  
Db 7 AHV--ANPQAEQOLWLNRRANALLANGVELRD-NQLVVPSEGLVYVSQVLFKQGGCP 63  
QY 71 -----CSNREASSQAPFIASLCLKSPGRFERILLRANTHSSAKPCQGSIHLCGV 121  
Db 64 STEMLLTHSISRIASVQAKVNLISAIKSP--CORETPRKAATNPMYEP-----IYLGV 116  
QY 122 FELQPG--ASVFNVTDPQSVSHGTGTSFGLL 152  
Db 117 FOLEKGDRLSAEINLPDYLDLAR-SQVYFGLI 148

## RESULT 3

Q9TTG7 PRELIMINARY; PRT; 138 AA.  
AC Q9TTG7;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE Tumor necrosis factor alpha (Fragment).  
GN TNF-ALPHA.  
OS Aotus lemurinus (Northern gray-necked night monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
OX NCBI\_TaxID=57175;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,  
RA Patario M.E.;  
RT "Aotus lemurinus gene for TNF alpha";  
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF097329; AAF21304.1; -.  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR00478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SMO0207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

OX NCBI\_TaxID=43147;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,  
RA Patario M.E.;  
RT "Aotus lemurinus gene for TNF alpha";  
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF097329; AAF21304.1; -.  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR00478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SMO0207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 138 AA; 15269 MW; 29275E8F4CD5068 CRC64;

Query Match 15.2%; Score 120.5; DB 6; Length 138;  
Best Local Similarity 29.6%; Pred. No. 8.7e-05;  
Matches 42; Conservative 19; Mismatches 56; Indels 25; Gaps 5;

QY 17 AHVSEASSKTTSTVLQMAEKGYTMSNNLVTLENGKQLTVKROGLYYIAQVTF----- 70  
Db 7 AHV--ANPQAEQOLWLNRRANALLANGVELRD-NQLVVPSEGLVYVSQVLFKQGGCP 63  
QY 71 -----CSNREASSQAPFIASLCLKSPGRFERILLRANTHSSAKPCQGSIHLCGV 121  
Db 64 STEMLLTHSISRIASVQAKVNLISAIKSP--CORETPRKAATNPMYEP-----IYLGV 116  
QY 122 FELQPGASVFNVTDPQSVSHG 143  
Db 117 FOLEKGDRLSAEINLPDYLDLG 138

## RESULT 4

Q97543 PRELIMINARY; PRT; 149 AA.  
AC Q97543;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE Tumor necrosis factor alpha (Fragment).  
GN TNF-ALPHA.  
OS Aotus nancymae (owl monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
OX NCBI\_TaxID=37293;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Echeverry S.J., Hernandez E., Moreno A., Patario M.E., Murillo L.A.;  
RT "Identification, cloning and sequencing of different interleukin genes  
in 4 Aotus species";  
RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF014513; AAD01539.1; -.  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR00478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SMO0207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match 14.9%; Score 118; DB 6; Length 149;  
Best Local Similarity 28.3%; Pred. No. 0.00018;  
Matches 43; Conservative 21; Mismatches 62; Indels 26; Gaps 6;

QY 17 AHVISEASSTSVLQMAEKGYTMSNNLVTLENGKOLTVKROGLYYTYAQTFF-----70  
 DB 7 AHVV--ANPQAEQOLQWLNRRANALLANGVELRD-NQLVPSGSLYITISQVLFKQCGCP 63  
 QY 71 -----CSNEASSQAPFISLCLKSPGFERILLRAANTHSSAKPCGQOQSHLGGV 121  
 DB 64 STHTVLLHTTISRJAVSYQTKVNLLSAIKSPCQ-----RTPPGAEAKP-WYEPITLGGV 116  
 QY 122 FELQPGASVFNVTDPDSQVSHG-TGFTSFGL 152  
 DB 117 FOLEKGDRLSAEINRDYIDFASGQVYFGIT 148

RESULT 5  
 Q95LE8 PRELIMINARY; PRT; 99 AA.  
 AC Q95LE8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE TNF\_alpha (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BLOOD;  
 RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;  
 RT "Semi-quantification of canine cytokine expression by one tube RT-PCR."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DB EMBL: AF327889; AAC26919.1; -  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR PROSITE: PS00251; TNF\_1; UNKNOWN\_1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT 99 99  
 SQ SEQUENCE 99 AA; 10760 MW; 3977AE499F00D7B0 CRC64;

Query Match 9.3%; Score 73.5; DB 6; Length 99;  
 Best local Similarity 38.9%; Pred. No. 4.5;  
 Matches 21; Conservative 7; Mismatches 23; Indels 3; Gaps 2;  
 QY 17 AHVISEASSTSVLQMAEKGYTMSNNLVTLENGKOLTVKROGLYYTYAQTFF 70  
 DB 15 AHVV--ANPQAEQOLQWLNRRANALLANGVELRD-NQLVPSGSLYITISQVLF 65

RESULT 6  
 Q02837 PRELIMINARY; PRT; 134 AA.  
 AC Q02837;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Putative Beta-1,3-glucanase, C terminal.  
 GN AT2G43660.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam U., Talion L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eissen J.A.,  
 RA Salberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."  
 RL Nature 402:761-768 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Lin X.  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC002333; AAB64040.1; -  
 SQ SEQUENCE 134 AA; 14848 MW; D043CF59E44F662D CRC64;

Query Match 9.2%; Score 72.5; DB 10; Length 134;  
 Best local Similarity 26.4%; Pred. No. 8.5;  
 Matches 32; Conservative 7; Mismatches 25; Indels 57; Gaps 6;  
 QY 66 AQTFCNREASSQAPFISLCLKSPGFERILLRAANTHSSAKP-----110  
 DB 4 AQIWF-----PHILLCTISVSGSFRRVNAQAPGQSCWCAKGPTRIKOLVKNIAN 53  
 QY 111 -CGQOSIHL-----GGV-----FELQPGASVFN-----VTPDS 138  
 DB 54 VCSNSVHCEVSEGGACYPILVNSASVVMVLYYQNGRQYKCDPFGSGIISVTPDS 113  
 QY 139 Q 139  
 DB 114 E 114

RESULT 7  
 Q9TTJ2 PRELIMINARY; PRT; 93 AA.  
 ID Q9TTJ2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Fas ligand (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Suzuki M., Oida S., Shimokawa H.;  
 RT "Bos taurus Fas ligand mRNA, partial cds."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB035802; BAA88403.1; -  
 DR HSSP: P06804; 2TNF.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR ProDom: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT 93 93  
 SQ SEQUENCE 93 AA; 10410 MW; 753B178699578008 CRC64;

Query Match 9.0%; Score 71; DB 6; Length 93;  
 Best local Similarity 28.6%; Pred. No. 7.6;  
 Matches 24; Conservative 18; Mismatches 28; Indels 14; Gaps 5;  
 QY 2 NSEFMKGQDNP-----QIAHVISEASSTSVLQMAEKGYTMSNNLVTLENGKOL 54  
 DB 11 SSLEKQIGHPSPESEKELKKAHLTGKLNRSIP-LEW-EDTYGIALVSGVYKKG-SL 67



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DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)
DE Tumor necrosis factor (Fragment).
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RENAL LYMPH NODE;
RA Rao U.R., Klei T.R.;
RT "cDNA Cloning of Gerbil Tumor Necrosis Factor by Polymerase Chain
RT Reaction."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF171082; AAD51322.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_ab.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_ab.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 11169 MW; 06B5AF2CAEB62C6C CRC64;

Query Match
Best Local Similarity 8.3%; Score 65.5; DB 11; Length 101;
Matches 19; Conservative 12; Mismatches 27; Indels 7; Gaps 4;

QY 7 OKGQGNQIAHNVSEASKTSYLVQW AEKGYTMSNNLTLENGKQITVKGQGLYYIV 65
Db 37 QNASDKP--VAHV--PNOVEQLWLSRRANALLANGMELRDN--QLVVPDGLVIV 90
QY 66 AQVTF 70
Db 91 SQVLF 95

RESULT 12
Q27978 PRELIMINARY; PRT; 104 AA.
AC Q27978;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, last annotation update)
DE TNFA (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLSTEIN;
RA Dietz A.B., Neibergs H.L., Kehrli M.E.;
RT "Development of a Bovine TNFA Single Strand Conformational
RT Polymorphism."
DL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U11040; AAA19573.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_ab.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_ab.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11662 MW; BCE0A76D9FFA44BD CRC64;

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Query Match
Best Local Similarity 8.1%; Score 64.5; DB 6; Length 104;
Matches 17; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 31 IQMAEKGYTMSNNLTLENGKQITVKGQGLYYIAQVTF 70
Db 13 LFWMDSYNALLMANGVKLED--NQLVVPADGLVITLSQVLF 51

RESULT 13
Q90WP9 PRELIMINARY; PRT; 88 AA.
AC Q90WP9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Pleurocetes platessa (Plaice).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Pleuronectes.
OX NCBI_TaxID=8262;
RN [1]
RP SEQUENCE FROM N.A.
RA Laing K.J., Zou J.J., Secombes C.J.;
RT "Sequence analysis of plaice TNF-alpha."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416943; CAC95226.1; -.
DR InterPro; IPR003636; TNF_ab.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_ab.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 9676 MW; A8ED6CF0AB5F23E9 CRC64;

Query Match
Best Local Similarity 8.1%; Score 64; DB 13; Length 88;
Matches 24; Conservative 11; Mismatches 21; Indels 44; Gaps 4;

QY 60 GLYYIAQVTF---CSNREA-----SSQAPFIATLCTKS 90
Db 1 GLTFVYSQASFSVSCSDDAEGKARGRLTSVSHIRWYAESMGKDSLMSAVNSACHVG 60

QY 91 PGRFERILLAAVNTSSAKPCGQ---QSHLGVFELQPG 127
Db 61 P-----TQDNRFPDGGQWYNATVLAQVFLNEG 88

RESULT 14
Q9S3B6 PRELIMINARY; PRT; 140 AA.
AC Q9S3B6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, last annotation update)
DE Muty protein (Fragment).
GN Muty.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=88-39;
RX MEDLINE=99255683; PubMed=10320570;
RA Achtmann M., Azuma T., Berg D.E., Ito Y., Morelli G., Pan Z.J.,
RA Suerbaum S., Thompson S., van der Ende A., van Doorn L.J.;
RT "Recombination and clonal groupings within Helicobacter pylori from

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RT different geographic regions."  
RL Mol. Microbiol. 32:459-470(1999).  
DR EMBL; AJ239649; CAB37760.1; -.  
DR HSSP; P17802; 1MUY.  
DR InterPro; IPR003265; Endo\_3c.  
DR InterPro; IPR003583; HHH\_1.  
DR Pfam; PF00730; HhH-GPD; 1.  
DR SMART; SM00478; ENDO3c; 1.  
DR SMART; SM00278; HhH; 1.  
FT NON TER 1 140  
FT NON TER 1 140  
SQ SEQUENCE 140 AA; 15733 MM; 3F3779C85566BCFF CRC64;

Query Match 8.1%; Score 64; DB 2; Length 140;  
Best Local Similarity 22.9%; Pred. No. 70;  
Matches 32; Conservative 17; Mismatches 47; Indels 44; Gaps 7;

QY 30 VLOWAEKGYTMSNLT-----VLENGKQLTVKROGLYIYAQVTFCSN-REA 76  
Db 24 LLLMRGLGYTSRAKLNKSAEICVKEHNSQLPNDYQSLKLPGLGAYTANAILCFGRK 83  
QY 77 SSGAPFIASLCLKSPGFERILRA-----ANTHSAPCCGQSIHLGCVFELPGASVFV 132  
Db 84 SA-----CVDA--NIKVLRLRLGLDPNIHAK-----DLQIKANEFL 118  
QY 133 NVTDPQOVSHGTGTSFGL 152  
Db 119 NINE--SFNNQALIDLAL 136

RESULT 15  
09K2E4 PRELIMINARY; PRT; 67 AA.  
AC 09K2E4;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)  
DE Hypothetical protein CP0063.  
GN CP0063.  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Ulteback T., Berry K., Bass S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Gwin M., Neilson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia  
RT pneumoniae AR39."  
RL Nucleic Acids Res. 28:1397-1406(2000).  
DR EMBL; AE002169; AAF37952.1; -.  
DR TIGR; CP0063; -.  
KM Hypothetical protein.  
SQ SEQUENCE 67 AA; 7307 MM; 44E2ADB207460B7D CRC64;

Query Match 8.0%; Score 63; DB 16; Length 67;  
Best Local Similarity 33.3%; Pred. No. 34;  
Matches 19; Conservative 13; Mismatches 19; Indels 6; Gaps 3;

QY 100 RAANTHSAPCCGQSIHLGCVFELPGASVFVNVTDPQOVSHGT--GFTSFGLKL 154  
Db 12 RAANTIVNTR--QKPFHGMATLRBNATSIINIKEDA-LSLGTGVSFASTASIKI 64

Search completed: June 7, 2003, 12:09:37  
Job time: 80 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2003, 11:55:18 ; Search time 18.2386 Seconds

(without alignments)  
1375.717 Million cell updates/sec

Title: US-09-579-548A-1

Perfect score: 1335

Sequence: 1 MIETRYNOTSPRSNATGLPIS.....TDPQVSHGTGFTSFGLLKL 261

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: PIR 73: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	261	2	153476
2	1176	88.1	261	2	S53090
3	1027.5	77.0	260	1	S21738
4	130.5	9.8	233	1	OMWUX
5	126.5	9.5	233	1	S22052
6	122.5	9.2	234	1	A25451
7	122	9.1	279	2	A53062
8	121	9.1	234	1	JO1344
9	119.5	9.0	281	2	I36707
10	118.5	8.9	306	2	I49139
11	118	8.8	193	2	S06192
12	117.5	8.8	235	2	I54490
13	114.5	8.6	185	2	S52715
14	114.5	8.6	233	1	S24642
15	114.5	8.6	244	2	A46066
16	114	8.5	232	1	S12606
17	114	8.5	234	1	JH0529
18	114	8.5	234	1	A49266
19	110.5	8.3	235	1	OMWUX
20	108.5	8.1	235	2	JU0029
21	104	7.8	233	2	S11688
22	97.5	7.3	1217	2	C86159
23	95.5	7.2	1817	2	H71611
24	95.5	7.2	2166	2	G70163
25	93	7.0	582	2	H97306
26	93	7.0	822	2	AB2507
27	92	6.9	305	2	S44661
28	91.5	6.9	1864	2	F86378
29	91	6.8	204	1	S24641

30	90.5	6.8	1080	2	S48961	hypothetical prote
31	89	6.7	197	1	JH0309	tumor necrosis fac
32	88.5	6.6	205	1	OMWUX	lymphotoxin alpha
33	88.5	6.6	401	2	T18285	hypothetical prote
34	88.5	6.6	1819	2	D97033	uncharacterized pr
35	88	6.6	204	1	S17289	tumor necrosis fac
36	87.5	6.6	613	2	H90160	conserved hypotet
37	87	6.5	668	2	JQ0774	penicillin-binding
38	87	6.5	668	2	T44118	hypothetical prote
39	87	6.5	887	2	T20866	hypothetical prote
40	87	6.5	1345	2	T00964	tumor necrosis fac
41	86.5	6.5	202	1	B27303	hypothetical prote
42	86.5	6.5	735	2	T41187	hypothetical prote
43	85.5	6.4	1001	2	H64593	type III restricti
44	84.5	6.3	620	2	AD1659	exonuclease ABC c
45	84.5	6.3	1042	2	S41705	EVII protein - hum

## ALIGNMENTS

## RESULT 1

153476

CD40 ligand - human

N/Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence, revision 02-Jul-1996 #text change 20-Apr-2001

C/Accession: S28017; JH0793; S26694; S2852; I53476; S25684; S30593

R/Hollenbaugh, D.; Gromaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.

EMBO J. 11, 4313-4321, 1992

A/Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand f

A/Reference number: S28017; MUID:93049181; PMID:1385114

A/Accession: S28017

A/Molecule type: mRNA

A/Residues: 1-261 <GRA>

A/Cross-references: EMBL:215017; NID:G38483; PIDN:CAA78737.1; PID:G38484

R/Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Cliford, K.N.; Macduff, B.M.; Sato,

J. Exp. Med. 176, 1543-1550, 1992

A/Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobu

A/Reference number: JH0793; MUID:930494757; PMID:1281209

A/Accession: JH0793

A/Molecule type: mRNA

A/Residues: 1-261 <SPR>

A/Cross-references: GB:X67878; NID:G38411; PIDN:CAA48077.1; PID:G38412

A/Experimental source: peripheral blood T-cell

R/Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Krocze, R.A.

Exp. J. Immunol. 22, 3191-3194, 1992

A/Title: Cloning of TRAP, a ligand for CD40 on human T cells.

A/Reference number: S26694; MUID:93076854; PMID:1280226

A/Accession: S26694

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-261 <GRA>

A/Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270

R/Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy,

FEBS Lett. 315, 259-266, 1993

A/Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of

A/Reference number: S28852; MUID:93138085; PMID:7678552

A/Accession: S28852

A/Molecule type: mRNA

A/Residues: 1-261 <GAU>

A/Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124

A/Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln

C/Genetics:

A/Gene: GDB:CD40LG; HIGM1; IMJ3

A/Cross-references: GDB:1120632; OMIM:308230

A/Map position: Xq26-Xq26

C/Keywords: glycoprotein; transmembrane protein

F/13-44/Domain: transmembrane #status predicted <TM>

F/45-261/Domain: extracellular #status predicted <EXT>

F/6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

100.0%; Score 1335; DB 2; Length 261;





A>Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A:Reference number: A44189; MUID:85142190; PMID:3856324  
A:Accession: A44189  
A:Molecule type: mRNA  
A:Residues: 1-62,'S','64'-233 <MAN>  
A:Cross-references: GB:M10988; NID:G339737; PIDN:AAA61198.1; PID:g339738  
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Maasaki, N.; Nakamura, K.I.; Arimura, H.  
Lymphokine Res. 7, 175-185, 1988  
A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and gamma by transfection of plasmids encoding their cDNAs into COS cells.  
A:Reference number: A61478; MUID:88301617; PMID:2841543  
A:Accession: B61478  
A:Molecule type: protein  
A:Residues: 83-102,109-119,121-128 'X', 130-131,142-144, 'X', 146, 'XXX', 150-152, 159-174, 180-181, 183-184, 186-187, 189-190, 192-193, 195-196, 198-199, 201-202, 204-205, 207-208, 210-211, 213-214, 216-217, 219-220, 222-223, 225-226, 228-229, 231-232, 234-235, 237-238, 240-241, 243-244, 246-247, 249-250, 252-253, 255-256, 258-259, 261-262, 264-265, 267-268, 270-271, 273-274, 276-277, 279-280, 282-283, 285-286, 288-289, 291-292, 294-295, 297-298, 300-301, 303-304, 306-307, 309-310, 312-313, 315-316, 318-319, 321-322, 324-325, 327-328, 330-331, 333-334, 336-337, 339-340, 342-343, 345-346, 348-349, 351-352, 354-355, 357-358, 360-361, 363-364, 366-367, 369-370, 372-373, 375-376, 378-379, 381-382, 384-385, 387-388, 390-391, 393-394, 396-397, 399-400, 402-403, 405-406, 408-409, 411-412, 414-415, 417-418, 420-421, 423-424, 426-427, 429-430, 432-433, 435-436, 438-439, 441-442, 444-445, 447-448, 450-451, 453-454, 456-457, 459-460, 462-463, 465-466, 468-469, 471-472, 474-475, 477-478, 480-481, 483-484, 486-487, 489-490, 492-493, 495-496, 498-499, 501-502, 504-505, 507-508, 510-511, 513-514, 516-517, 519-520, 522-523, 525-526, 528-529, 531-532, 534-535, 537-538, 540-541, 543-544, 546-547, 549-550, 552-553, 555-556, 558-559, 561-562, 564-565, 567-568, 570-571, 573-574, 576-577, 579-580, 582-583, 585-586, 588-589, 591-592, 594-595, 597-598, 600-601, 603-604, 606-607, 609-610, 612-613, 615-616, 618-619, 621-622, 624-625, 627-628, 630-631, 633-634, 636-637, 639-640, 642-643, 645-646, 648-649, 651-652, 654-655, 657-658, 660-661, 663-664, 666-667, 669-670, 672-673, 675-676, 678-679, 681-682, 684-685, 687-688, 690-691, 693-694, 696-697, 699-700, 702-703, 705-706, 708-709, 711-712, 714-715, 717-718, 720-721, 723-724, 726-727, 729-730, 732-733, 735-736, 738-739, 741-742, 744-745, 747-748, 750-751, 753-754, 756-757, 759-760, 762-763, 765-766, 768-769, 771-772, 774-775, 777-778, 780-781, 783-784, 786-787, 789-790, 792-793, 795-796, 798-799, 801-802, 804-805, 807-808, 810-811, 813-814, 816-817, 819-820, 822-823, 825-826, 828-829, 831-832, 834-835, 837-838, 840-841, 843-844, 846-847, 849-850, 852-853, 855-856, 858-859, 861-862, 864-865, 867-868, 870-871, 873-874, 876-877, 879-880, 882-883, 885-886, 888-889, 891-892, 894-895, 897-898, 900-901, 903-904, 906-907, 909-910, 912-913, 915-916, 918-919, 921-922, 924-925, 927-928, 930-931, 933-934, 936-937, 939-940, 942-943, 945-946, 948-949, 951-952, 954-955, 957-958, 960-961, 963-964, 966-967, 969-970, 972-973, 975-976, 978-979, 981-982, 984-985, 987-988, 990-991, 993-994, 996-997, 999-1000, 1002-1003, 1005-1006, 1008-1009, 1011-1012, 1014-1015, 1017-1018, 1020-1021, 1023-1024, 1026-1027, 1029-1030, 1032-1033, 1035-1036, 1038-1039, 1041-1042, 1044-1045, 1047-1048, 1050-1051, 1053-1054, 1056-1057, 1059-1060, 1062-1063, 1065-1066, 1068-1069, 1071-1072, 1074-1075, 1077-1078, 1080-1081, 1083-1084, 1086-1087, 1089-1090, 1092-1093, 1095-1096, 1098-1099, 1101-1102, 1104-1105, 1107-1108, 1110-1111, 1113-1114, 1116-1117, 1119-1120, 1122-1123, 1125-1126, 1128-1129, 1131-1132, 1134-1135, 1137-1138, 1140-1141, 1143-1144, 1146-1147, 1149-1150, 1152-1153, 1155-1156, 1158-1159, 1161-1162, 1164-1165, 1167-1168, 1170-1171, 1173-1174, 1176-1177, 1179-1180, 1182-1183, 1185-1186, 1188-1189, 1191-1192, 1194-1195, 1197-1198, 1199-1200, 1202-1203, 1205-1206, 1208-1209, 1211-1212, 1214-1215, 1217-1218, 1220-1221, 1223-1224, 1226-1227, 1229-1230, 1232-1233, 1235-1236, 1238-1239, 1241-1242, 1244-1245, 1247-1248, 1250-1251, 1253-1254, 1256-1257, 1259-1260, 1262-1263, 1265-1266, 1268-1269, 1271-1272, 1274-1275, 1277-1278, 1280-1281, 1283-1284, 1286-1287, 1289-1290, 1292-1293, 1295-1296, 1298-1299, 1301-1302, 1304-1305, 1307-1308, 1310-1311, 1313-1314, 1316-1317, 1319-1320, 1322-1323, 1325-1326, 1328-1329, 1331-1332, 1334-1335, 133

CY

	Query Match	9.8%	Score 130.5;	DB 1;	Length 233;
	Best Local Similarity	27.4%;	Pred. No. 0.0014;		
	Matches	54;	Conservative	26;	Mismatches 88;
				Indels	29;
				Gaps	7;
81	L N C E E I K S O F E G V K D I M L N K E T K E N S P E M Q X G O O P I A H V I S S A S K T T S V L W				
:	:   :	:	:	:	:

```

QY      141 AERGVYTMNNVLVTLENGKQLTVKRGGLYYIAQVTF-----VAHV--ANPQAEGLQW 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      105 LNRRAALLANGVELRD-NQLVVPSSBGLYLLISQVLFKQGCPSSTVLLTHTTISRIVASY 163
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      186 QAPFIASLCLKSPGRFERILLPAANTHSSAKPCGQOSIHAGVFELQPGASVFNVTDPDS 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      164 QTKVNLISAIKSPCQ-----RETPEGAKAK-WPEPIYLGGVFQLEKGRLSAEINRPD 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      246 QVSHG-TGFTSFGLLKL 261
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      217 YLDFPAGSGQVYFGIALL 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
S22052
tumor necrosis factor alpha precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S22052
R:Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A:Reference number: S22052
A:Accession: S22052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <SAN>
A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C:Genetics:
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:13/20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match          9.5%; Score 126.5; DB 1; Length 233;
Best Local Similarity 27.9%; Pred. No. 0.0031;
Matches 55; Conservative 24; Mismatches 89; Indels 29; Gaps 7;

QY      81 LANCEIKQKQFEGFVQDMLNKEETKENSFEMOKGDONPOIAHVISEASSKTTSVLQW 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      50 LHFEGVIGPQREFFPPDPLISPLAQAVSSSRTPSDKP---VAHV--ANPQAEGLQW 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      141 AERGVYTMNNVLVTLENGKQLTVKRGGLYYIAQVTF-----CSNRBAS 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      105 LNRRAALLANGVELRD-NQLVVPSSBGLYLLISQVLFKQGCPSSTVLLTHTTISRIVASY 163
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      186 QAPFIASLCLKSPGRFERILLPAANTHSSAKPCGQOSIHAGVFELQPGASVFNVTDPDS 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      164 QTKVNLISAIKSPCQ-----RETPEGAKAK-WPEPIYLGGVFQLEKGRLSAEINLPD 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      246 QVSHG-TGFTSFGLLKL 261
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      217 YLDFPAGSGQVYFGIALL 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
A25451
tumor necrosis factor alpha precursor - rabbit
M:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25454; A25451; J60727
R:Itto, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, F.
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for ra
A:Reference number: A25454; MUID:86219711; PMID:3519137
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <ITMO>

```

RESULT 6  
A25451  
tumor necrosis factor alpha precursor - rabbit  
N.Alternate names: cachectin; TNF alpha  
C.Species: Oryctolagus cuniculus (domestic rabbit)  
C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 04-Feb-2000  
C.Accession: A25454; A25451; J050727  
R.Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, F.  
DNA 5, 149-156, 1986  
A.Title: Molecular cloning and expression in *Escherichia coli* of the cDNA coding for rat  
A.Reference number: A25454; MUID:86219711; PMID:3519137  
A.Accession: A25454  
A.Molecule type: mRNA  
A.Residues: 1-234 <ITO>

A/Cross-references: GB:M12845; NID:9165759; PIDN:AAA11486.1; PID:9165760  
 R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
 DNA 5, 157-165, 1996  
 A/Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
 A/Reference number: A25451; MUID:86219712; PMID:3519138  
 A/Accession: A25451  
 A/Molecule type: DNA  
 A/Residues: 1-234 <IT>  
 A/Note: This sequence differs from that shown in having a Gln inserted between residues  
 R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
 Gene 95, 215-221, 1990  
 A/Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-  
 A/Reference number: J03009; MUID:91065534; PMID:2249779  
 A/Accession: J03027  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-62, 'Q', 63-234 <SHA>  
 A/Cross-references: GB:M60340; GB:M5326; NID:9165754; PIDN:AAA31484.1; PID:9165756  
 C/Genetics:  
 A/Intons: 62/3; 80/1; 96/1  
 C/Superfamily: tumor necrosis factor  
 C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; men  
 F:1-61/Domains: propeptide #status predicted <PRO>  
 F:82-234/Product: tumor necrosis factor #status predicted <MAT>  
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:83/Binding site: carboxylate (Ser) (covalent) #status predicted  
 F:147-178/Disulfide bonds: #status predicted

Query Match 9.2%; Score 122.5; DB 1; Length 234;  
 Best Local Similarity 28.8%; Pred. No. 0.0068;  
 Matches 44; Conservative 24; Mismatches 60; Indels 25; Gaps 7;

OY 124 AHVSESSKTSYLOW-AEKGYYTMSNLTLENGKQLYTKRQGLYYIAQVTFCSNRE 182  
 Db 92 AHVV--ANPQVEGQLQWISQANALNAGMLTNN--QLVVPADGLYIYSQVLF----- 142

OY 183 ASSQAPFIASICLSPGRFERILLRANTHSSAK-PCGQOS-----IHLGVP 229  
 Db 143 -SGGCGRSYVLLHTHTVERFANYSYPMXNLSAITSFCHREPEAEPMATEPIYILGQVF 201

OY 230 ELQPGASVFNVTDPQVSHG-TGFTSPGLLKL 261  
 Db 202 QLEKGRLLSTEVNQPEYILDALSGQVYFGIALL 234

RESULT 7  
 A53062  
 Fas ligand - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C/Accession: A53062  
 R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag  
 Cell 76, 969-976, 1994  
 A/Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in  
 A/Reference number: A53062; MUID:94185175; PMID:7511063  
 A/Accession: A53062  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-279 <TKA>  
 A/Cross-references: GB:U06948; NID:9473564; PIDN:AAA17800.1; PID:9473565

Query Match 9.1%; Score 122; DB 2; Length 279;  
 Best Local Similarity 24.0%; Pred. No. 0.0094;  
 Matches 55; Conservative 37; Mismatches 101; Indels 36; Gaps 9;

OY 50 LDKIEERNLHDFV-FMKTICQNTGERSLSLNCBEIKSQEPGVVKQIMNKERTKKE 108  
 Db 70 LKKKHNTMLMPLVFFFMVLVAGLQYQLFHLQKEIAELREFT-----NOSLTV 122

OY 109 NSPEWQKD-----QNFOIAHVISSEASKTSYLOWAEKGYTMSNLTLENGKQL 161  
 Db 123 SSFEKQIANPSTPESEKPEPSVAHLGNHRSRIP-LEM-EDTYGALISGVYKKG-GL 179

OY 162 TVKRGGLYYIAQVTF-----CSNREASQ-----APFIASICLSPGRFERILLRANTH 212  
 Db 180 VINENGLYFVYSKYFFFGQSCNNQPLNKHVYMRNSKIPEDVLWBEKRLNCTTGQIWAH 239

OY 213 SSAPPCGQOSIHLGVEFELQPGASVFNVTDPQVSHG-TGFTSPGLLKL 261  
 Db 240 SS-----YLGAVFNLTSADHLVYNISQLSLINEESKTPFGLYL 279

RESULT 8  
 J01344  
 tumor necrosis factor alpha precursor - horse  
 N/Alternate names: cachectin; TNF alpha  
 C/Species: Equus caballus (domestic horse)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 A/Accession: J01344  
 R:Su, X.; Morris, D.D.; McGraw, R.A.  
 Gene 107, 319-321, 1991  
 A/Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis  
 A/Reference number: J01344; MUID:92084125; PMID:1748301  
 A/Accession: J01344  
 A/Molecule type: DNA  
 A/Residues: 1-234 <STX>  
 A/Cross-references: GB:M64087; NID:9164244; PIDN:AAA30959.1; PID:9164245  
 C/Comment: This protein is an important proximal mediator of endotoxemia.  
 C/Genetics:  
 A/Gene: TNF-alpha  
 A/Intons: 62/3; 79/1; 95/1  
 C/Superfamily: tumor necrosis factor  
 C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; men  
 F:18-234/Product: tumor necrosis factor alpha #status predicted <TNF>  
 F:79,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F:82/Binding site: carboxylate (Ser) (covalent) #status predicted  
 F:146-178/Disulfide bonds: #status predicted

Query Match 9.1%; Score 121; DB 1; Length 234;  
 Best Local Similarity 25.7%; Pred. No. 0.0091;  
 Matches 47; Conservative 35; Mismatches 71; Indels 30; Gaps 10;

OY 102 KEETKENSFE-----MOKGDQNP--QIAHVISSEASKTSYLOW-AEKGYYTMSN 150  
 Db 59 QREQEPNMFQSTNPLAQTLRSSRTPSDPAHV--ANPQVEGQLQWISQANALN 116

OY 151 NLVTLENGKQLYTKRQGLYYIAQVTFCSNREASQAPF---IASICLSPGRFERILLR 207  
 Db 117 GVALTDN--QLVVPDLGLYIYSQVLFKGGGCPSTHLLTHTISRLAVSPKVN--LLS 172

OY 208 AANT-----HSSAKPCGQOSIHLGVEFELQPGASVFNVTDPQVSHG-TGFTSPGL 258  
 Db 173 AIKSPCHTESPQAEAKP-WYEPYIYAGVLEKQDQLSARINQPNYLDPAESGQVYFGI 231

OY 259 LKL 261  
 Db 232 IAL 234

RESULT 9  
 I38707  
 Fas ligand - human  
 C/Species: Homo sapiens (man)  
 C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
 C/Accession: I38707; J02340; S57565; I38554  
 R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
 Int. Immunol. 6, 1567-1574, 1994  
 A/Title: Human Fas ligand: gene structure, chromosomal location and species specificity  
 A/Reference number: I38707; MUID:95127560; PMID:7826947  
 A/Accession: I38707  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-281 <RBS>  
 A/Cross-references: EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431  
 R:Ito, H.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.  
 Biochem. Biophys. Res. Commun. 204, 468-474, 1994





Sat Jun 7 12:24:13 2003

us-09-579-548a-1.rpr

Page 7

Oy 212 ---HSSAKPCGQOSIHGVEFELOPGASVFVNVTDPQVSHGTGFTSPG 257  
Db 191 PARQGYGPLMYTSVFGGLVOLRRGERVYVNI SHPDWVDFARGKTFFG 239

Search completed: June 7, 2003, 12:00:30  
Job time : 20.2386 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2003, 11:55:14 ; Search time 16.3518 Seconds

(without alignments)  
662.026 Million cell updates/sec

Title: US-09-579-548A-1

Sequence: 1 MIETNOTSPRSAAATGIPIS.....TDPQVSHGTGFTSFGILKL 261

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	1335	100.0	261	1	TNFS_HUMAN
2	1316	98.6	261	1	TNFS_MACMU
3	1301	97.5	261	1	TNFS_AOTTR
4	1297	97.2	261	1	TNFS_CALJA
5	1183.5	88.7	240	1	TNFS_MACNE
6	1176	88.1	261	1	TNFS_BOVIN
7	1150	86.1	261	1	TNFS_PIG
8	1138.5	85.3	260	1	TNFS_FELCA
9	1112.5	83.3	260	1	TNFS_CANRA
10	1031.5	77.3	260	1	TNFS_MOUSE
11	1020.5	76.4	260	1	TNFS_MOUSE
12	477.5	35.8	272	1	TNFS_RAT
13	175.5	13.1	318	1	TNFI_RAT
14	171.5	12.8	316	1	TNFI_MOUSE
15	158.5	11.9	317	1	TNFI_HUMAN
16	147.5	11.0	281	1	TNFI_HUMAN
17	145.5	10.9	291	1	TNFI_MOUSE
18	133.5	10.0	233	1	TNFA_MARMO
19	130.5	9.8	233	1	TNFA_HUMAN
20	126.5	9.5	233	1	TNFA_PAPSP
21	126	9.4	310	1	TNFC_MARMO
22	125.5	9.4	233	1	TNFA_MACRA
23	125.5	9.4	233	1	TNFA_MACMU
24	122.5	9.2	235	1	TNFA_MACMU
25	122	9.1	279	1	TNFA_RABIT
26	121.5	9.1	233	1	TNFA_MOUSE
27	121	9.1	233	1	TNFA_PAPHU
28	121	9.1	233	1	TNFA_DBLIE
29	121	9.1	233	1	TNFA_TURTR
30	119.5	9.0	233	1	TNFA_HORSE
31	119.5	9.0	234	1	TNFA_MACEU
32	119.5	9.0	234	1	TNFA_CAVPO
33	118.5	8.9	280	1	TNFI_HUMAN
					TNFI_MACMU

## ALIGNMENTS

RESULT 1	TNFS_HUMAN	STANDARD;	PRT;	261 AA.
ID	TNFS_HUMAN			
AC	P29965;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-l) (TNF-related activation protein) (TRAP) (T cell antigen gp39) (CD134 antigen).			
GN	TNFSFS OR CD40LG OR CD40L OR TRAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93076854; PubMed=1280226;			
RA	Graf D., Korthauer U., Mages H.W., Senger G., Kroczeck R.A.;			
RT	"Cloning of TRAP, a ligand for CD40 on human T cells.";			
RL	Bur. J. Immunol. 22:3191-3194(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93049181; PubMed=1385114;			
RA	Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,			
RA	Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,			
RA	Aruffo A.;			
RT	"The human T cell antigen gp39, a member of the TNF gene family, is a			
RT	ligand for the CD40 receptor: expression of a soluble form of gp39			
RT	with B cell co-stimulatory activity.";			
RL	EMBO J. 11:4313-4321(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.			
RX	MEDLINE=93145330; PubMed=7678782;			
RA	Aruffo A., Farrington M., Hollenbaugh D., Li X., Milstovich A.,			
RA	Nonoyama S., Bagjorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,			
RA	Robertson R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;			
RT	"The CD40 ligand, gp39, is defective in activated T cells from			
RT	patients with X-linked hyper-Igm syndrome.";			
RL	Cell 72:291-300(1993).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93094757; PubMed=1281209;			
RA	Springer M.K., Armitage R.J., Strockbine L., Clifford K.N.,			
RA	Macduff B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;			
RT	"Recombinant human CD40 ligand stimulates B cell proliferation and			
RT	immunoglobulin E secretion.";			
RL	J. Exp. Med. 176:1543-1550(1992).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93138085; PubMed=7678552;			
RA	Gauchat J.F.M., Aubry J., Mazzel G.J., Life P., Domotte T., Eison G.,			
RA	Bonney J.Y.;			
RT	"Human CD40-ligand: molecular cloning, cellular distribution and			
RT	regulation of expression by factors controlling Ige production.";			
RL	FEBS Lett. 315:259-266(1993).			

34	118.5	8.9	306	1	TNFC_MOUSE	P4155	mus musculus
35	117.5	8.8	235	1	TNFA_PERLE	P36939	peromyscus
36	117	8.8	233	1	TNFA_CANFA	P51742	capra famli
37	116.5	8.7	234	1	TNFA_CAPHI	P3326	capra hircu
38	116.5	8.7	280	1	TNFC_CERTO	Q9bdn1	cercocebus
39	114.5	8.6	233	1	TNFA_BOVIN	Q06599	bos taurus
40	114.5	8.6	244	1	TNFC_HUMAN	Q06643	homo sapien
41	114.5	8.6	282	1	TNFC_PIG	Q9bea8	sus scrofa
42	114	8.5	232	1	TNFA_PIG	P23563	sus scrofa
43	114	8.5	234	1	TNFA_SHEEP	P23383	ovis aries
44	114	8.5	278	1	TNFC_RAT	P36940	rattus norv
45	111	8.3	150	1	TNFC_PIG	Q9tsv8	sus scrofa





Query Match 100.0%; Score 1335; DB 1; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-107;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPSAATGPIISKIFMYLTLVFLITOMIGSALFAYVLRRLKIEDERLH 60  
 DB 1 MIETYNQTSPPSAATGPIISKIFMYLTLVFLITOMIGSALFAYVLRRLKIEDERLH 60  
 QY 61 EDFVFMKTICRNTGERSLSLNCBEEKISQEGFVYKDIMLKEETKENSFEMQKQDNP 120  
 DB 61 EDFVFMKTICRNTGERSLSLNCBEEKISQEGFVYKDIMLKEETKENSFEMQKQDNP 120  
 QY 121 QIAAHVISEASSKTSVYLQMAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTCNS 180  
 DB 121 QIAAHVISEASSKTSVYLQMAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTCNS 180  
 QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGCVFELQPGASVFN 240  
 DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGCVFELQPGASVFN 240  
 QY 241 VTDPQVSHGTGFTSFGLLKL 261  
 DB 241 VTDPQVSHGTGFTSFGLLKL 261

RESULT 2  
 TNFS\_MACMU STANDARD; PRT; 261 AA.  
 AC 09BDC7;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-  
 L) (CD154 protein).  
 GN TNFS5 OR CD40LG OR CD40L.  
 OS Macaca mulatta (Rhesus macaque), and  
 OC Cercopithecus torquatus atys (Red-crowned mangabey) (scooby mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544, 9531;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND M.MULATTA VARIANTS GUN-60; VAL-204; PRO-206  
 RP AND THR-215.  
 RC SPECIES=M.mulatta, and C.torquatus atys; TISSUE=Lymphocytes;  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostrick P., Wayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing and homology analysis of nonhuman primate  
 RT Fas/Fas-ligand and co-stimulatory molecules";  
 RL Immunogenetics 53:315-328(2001)  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell  
 CC proliferation in the absence of co-stimulus as well as IGF  
 CC production in the presence of IL-4. Involved in immunoglobulin  
 CC class switching (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
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 CC  
 CC EMBL; AF344859; AAK37541.1; -  
 CC EMBL; AF344841; AAK37600.1; -  
 DR

DR HSP; P23965; 1ALY.  
 DR InterPro; IPR003263; TNF\_5.  
 DR InterPro; IPR003636; TNF\_abc.  
 DR InterPro; IPR00478; TNF\_family.  
 DR Pfam; PF00229; TNF\_1.  
 DR ProDom; PD002012; TNF\_abc; 1.  
 DR SMART; SM00207; TNF\_1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KM Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Polymorphism.  
 FT CHAIN 1 261  
 FT CHAIN 113 261  
 FT DOMAIN 1 22  
 FT TRANSMEM 23 43  
 FT DOMAIN 44 261  
 FT SITE 112 113  
 FT DISULFID 178 218  
 FT CARBOHYD 240 240  
 FT VARIANT 60 60  
 FT VARIANT 204 204  
 FT VARIANT 206 206  
 FT VARIANT 215 215  
 SQ SEQUENCE 261 AA; 29366 MW; AA2E0F11C0F28AB8 CRC64;

Query Match 98.6%; Score 1316; DB 1; Length 261;  
 Best Local Similarity 98.1%; Pred. No. 5.7e-106;  
 Matches 256; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPSAATGPIISKIFMYLTLVFLITOMIGSALFAYVLRRLKIEDERLH 60  
 DB 1 MIETYNQTSPPSAATGPIISKIFMYLTLVFLITOMIGSALFAYVLRRLKIEDERLH 60  
 QY 61 EDFVFMKTICRNTGERSLSLNCBEEKISQEGFVYKDIMLKEETKENSFEMQKQDNP 120  
 DB 61 EDFVFMKTICRNTGERSLSLNCBEEKISQEGFVYKDIMLKEETKENSFEMQKQDNP 120  
 QY 121 QIAAHVISEASSKTSVYLQMAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTCNS 180  
 DB 121 QIAAHVISEASSKTSVYLQMAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTCNS 180  
 QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGCVFELQPGASVFN 240  
 DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGCVFELQPGASVFN 240  
 QY 241 VTDPQVSHGTGFTSFGLLKL 261  
 DB 241 VTDPQVSHGTGFTSFGLLKL 261

RESULT 3  
 TNFS\_AOTTR STANDARD; PRT; 261 AA.  
 AC 09BDC7;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-  
 L) (CD154 protein).  
 GN TNFS5 OR CD40LG OR CD40L.  
 OS Aotus trivirgatus (Night monkey) (Douroucouli).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 NCBI\_TaxID=9505;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Lymphocytes;  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostrick P., Wayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;

```
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RT Immunogenetics 53:315-328(2001).
CC -|- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -|- SUBUNIT: HOMOTRIMER (By similarity).
CC -|- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -|- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: AF344860; AAK37542.1; -
DR HSSP: P29965; 1ALY.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.
DR PROSITE: PS0049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT
FT CHAIN 113 261
FT
FT DOMAIN 1 22
FT
FT TRANSMEM 23 43
FT
FT DOMAIN 44 261
FT
FT SITE 112 113
FT
FT DISULFID 178 218
FT
FT CARBOHYD 240 240
FT
FT SEQUENCE 261 AA; 29357 MW; 85E1588B507901B5 CRC64;
SQ
Query Match 97.5%; Score 1301; DB 1; Length 261;
Best Local Similarity 96.6%; Pred. No. 1.1e-104;
Matches 252; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 METYNQTSRPSAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRRLDKIEDERNH 60
DB 1 MEETHQAPRPSAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRRLDKIEDERNH 60
QY 61 EEFVPMKTIQRNCTGERSLILNCEIKSQEFGFKDMLNTEERKNSPEMOKGDNP 120
DB 61 EEFVPMKTIQRNCTGERSLILNCEIKSQEFGFKDMLNTEERKNSPEMOKGDNP 120
QY 121 QIAAHVISEASAKTTSVLOMAEKGYTMSNNLVTLNKGKQLTVKRGGLYYIYAQVTPCSN 180
DB 121 QIAAHVISEASAKTTSVLOMAEKGYTMSNNLVTLNKGKQLTVKRGGLYYIYAQVTPCSN 180
QY 121 QIAAHVISEASAKTTSVLOMAEKGYTMSNNLVTLNKGKQLTVKRGGLYYIYAQVTPCSN 180
DB 121 QIAAHVISEASAKTTSVLOMAEKGYTMSNNLVTLNKGKQLTVKRGGLYYIYAQVTPCSN 180
QY 181 REASSQAPPIALCLCKPFRFRIILRAANTHSSAKPGQOOSIHGVPFELQPGASVFN 240
DB 181 REASSQAPPIALCLCKPFRFRIILRAANTHSSAKPGQOOSIHGVPFELQPGASVFN 240
QY 241 VTDPSOVSHGTGFTSFGLLKL 261
DB 241 VTDPSOVSHGTGFTSFGLLKL 261
RESULT 4
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TNFS_CALJA STANDARD; PRT; 261 AA.
AC Q9BDN3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L) (CD154 protein).
GN TNFSF5 OR CD40LG OR CD40L.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callitrix.
OX NCBI_taxid=9483;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RT Immunogenetics 53:315-328(2001).
CC -|- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -|- SUBUNIT: HOMOTRIMER (By similarity).
CC -|- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -|- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF344864; AAK37603.1; -
DR HSSP: P29965; 1ALY.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT
FT CHAIN 113 261
FT
FT DOMAIN 1 22
FT
FT TRANSMEM 23 43
FT
FT DOMAIN 44 261
FT
FT SITE 112 113
FT
FT DISULFID 178 218
FT
FT CARBOHYD 240 240
FT
FT SEQUENCE 261 AA; 29360 MW; 10CA58B9237545B CRC64;
SQ
Query Match 97.2%; Score 1297; DB 1; Length 261;
Best Local Similarity 96.9%; Pred. No. 2.5e-104;
Matches 253; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 METYNQTSRPSAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRRLDKIEDERNH 60
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Db      1 MIETNQPSPRSATGHPISMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERMLH 60
Qy      61 EDFVPMKTIORCNTGERSLSLNCBEEKSQFEGFVKDMLNKEFTKENSFEMOKGQNP 120
Db      61 EDFVPMKTIORCNTGERSLSLNCBEEKSQFEGFVKDMLNKEFTKENSFEMOKGQNP 120
Qy      121 QIAAHVISEASKTTSVLQMAEKYTTMSNNLVTLNKGKLTVRKQGLYYIYAQVTFCSN 180
Db      121 QIAAHVISEASKTTSVLQMAEKYTTMSNNLVTLNKGKLTVRKQGLYYIYAQVTFCSN 180
Qy      181 REASSQAPFIASLCLKSPGPERFILLRAANTHSSAKPGQOSIHLGAVFELQPGASVFN 240
Db      181 REASSQAPFIASLCLKSPGPERFILLRAANTHSSAKPGQOSIHLGAVFELQPGASVFN 240
Qy      241 VTDPQVSHGTGFTSFGLLKL 261
Db      241 VTDPQVSHGTGFTSFGLLKL 261

```

## RESULT 5

```

TNFS_MACNE STANDARD; PRT; 240 AA.
ID TNFS_MACNE
AC Q9BDM7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
  l) (CD154 protein).
GN TNFSF5 OR CD40LG OR CD40L.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
  Fas/Fas-ligand and co-stimulatory molecules.";
RT Immunogenetics 53:315-328(2001).
RL -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
  proliferation in the absence of co-stimulus as well as IGE
  production in the presence of IL-4. Involved in immunoglobulin
  class switching (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
  extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
  proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; AF344853; AAK37613.1;
DR HSSP; P29965; IALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.

```

```

KM Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 240
FT CHAIN 1 240
FT CHAIN 113 240
FT CHAIN 23 43
FT DOMAIN 1 22
FT TRANSMEM 23 43
FT DOMAIN 44 240
FT SITE 112 113
FT DISULFID 173 197
FT CARBOHYD 219 219
FT SEQUENCE 240 AA; 27273 MW; BAE6AA0213CAEDECCRC64;
Query Match 88.7%; Score 1183.5; DB 1; Length 240;
Best Local Similarity 89.3%; Pred. No. 1.3e-94;
Matches 233; Conservative 3; Mismatches 4; Indels 21; Gaps 1;

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Qy      1 MIETNQPSPRSATGHPISMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERMLH 60
Db      1 MIETNQPSPRSATGHPISMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERMLH 60
Qy      61 EDFVPMKTIORCNTGERSLSLNCBEEKSQFEGFVKDMLNKEFTKENSFEMOKGQNP 120
Db      61 EDFVPMKTIORCNTGERSLSLNCBEEKSQFEGFVKDMLNKEFTKENSFEMOKGQNP 115
Qy      121 QIAAHVISEASKTTSVLQMAEKYTTMSNNLVTLNKGKLTVRKQGLYYIYAQVTFCSN 180
Db      116 -----VLQMAEKGYTMSNNLVTLNKGKLTVRKQGLYYIYAQVTFCSN 159
Qy      181 REASSQAPFIASLCLKSPGPERFILLRAANTHSSAKPGQOSIHLGAVFELQPGASVFN 240
Db      160 REASSQAPFIASLCLKSPGPERFILLRAANTHSSAKPGQOSIHLGAVFELQPGASVFN 219
Qy      241 VTDPQVSHGTGFTSFGLLKL 261
Db      220 VTDPQVSHGTGFTSFGLLKL 240

```

## RESULT 6

```

TNFS_BOVIN STANDARD; PRT; 261 AA.
ID TNFS_BOVIN
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
  related activation protein) (TRAP) (T cell antigen GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=9606582; PubMed=7590981;
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
  and tumor necrosis factor alpha.";
RT Immunogenetics 42:430-433(1995).
RL -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
  proliferation in the absence of co-stimulus as well as IGE
  production in the presence of IL-4. Involved in immunoglobulin
  class switching (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
  EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: The soluble form derives from the membrane form by
  proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----

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	CC	or send an email to <a href="mailto:license@isb-stb.ch">license@isb-stb.ch</a> ).
	DR	EMBL; Z48469; CAA8363.1; -
	DR	HSSP; P29965; ITALY.
	DR	InterPro; IPR003263; TNF_5.
	DR	InterPro; IPR003636; TNF_abc.
	DR	InterPro; IPR000478; TNF_family.
	DR	Pfam; PF00229; TNF; 1.
	DR	ProDom; PD008600; TNF_5; 1.
	DR	SMART; SMO0207; TNF; 1.
	DR	PROSITE; PS00251; TNF_1; 1.
	DR	PROSITE; PS50049; TNF_2; 1.
	KM	Cyclokinin; Transmembrane; Glycoprotein; Signal-anchor.
	FT	CHAIN 1 261
	FT	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
	FT	MEMBER 5, MEMBRANE FORM.
	FT	CHAIN 113 261
	FT	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
	FT	MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
	FT	CYTOSOLSMIC (POTENTIAL).
	FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
	FT	(POTENTIAL).
	FT	DOMAIN 47 261
	FT	EXTRACELLULAR (POTENTIAL).
	FT	SITE 112 113
	FT	CLEAVAGE (BY SIMILARITY).
	FT	DISELFLD 178 218
	FT	POTENTIAL.
	FT	CAROHND 240 240
	FT	N-LINKED (GLCNAC...) (POTENTIAL).
	SO	SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;
	Query Match	88.1%; Score 1176; DB 1; Length 261;
	Best Local Similarity	88.5%; Pred. No. 6.2e-94;
	Matches 231; Conservative	7; Mismatches 23; Indels 0; Gaps 0;
Qy	1	MIEFYNOTSPRSAATGELPIKIMIKMYLLVTLITOMIGSLFAVYLHRLRDLKIEDERNLH 60
Db	1	MIETYSQSPRSVAVTGPVSKIKIMYLLVFLITOMIGSLFAVYLHRLRDLKIEDERNLH 60
Qy	61	EDFFPMKTIOQCNTGESELSLNCEBEIKSQPEGFVKDIMLNKEETKKENSFENOKDONP 120
Db	61	EDFFPMKTIOQCNGEGSLSLNCEBEIRSFEDIIVDKIMONKEEVKKKEKFEMHKDOEP 120
Qy	121	QIAAHVISEASAKTTSTVLONAKEYGYMTSNMLVTLENGKQLTKRGQLYYTYAQVTFCSN 180
Db	121	QIAAHVISEASSKTTSTVLONAPKYIYTLNNLVLTLENGKLAVKRGGFYIYYQVTFCSN 180
Qy	181	REASSQAFLIASLCIKSPGRFERILLTAANTHTSSAKPCGQGSIIHLGVFELOPGASVPFN 240
Db	181	RELTSQAFLIASLCIKSPSGSERILLRAANTHTSSSRFCQGSIIHLGVFELOGASVPFN 240
Qy	241	VTDPSQVSHGTGTFSGELKL 261
Db	241	VTDPSQVSHGTGTFSGELKL 261
<hr/>		
RESULT 7		
TNFS_PIG	TNFS_PIG	STANDARD; PRT; 261 AA.
AC Q95MO5;		
DT 15-JUN-2002 (Rel. 41, Created)		
DT 15-JUN-2002 (Rel. 41, Last sequence update)		
DT 15-JUN-2002 (Rel. 41, Last annotation update)		
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-		
DE L) (CD154 protein).		
GN TNFSF5 OR CD40LG OR CD40L.		
OS Sus scrofa (pig).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX NCBI_TaxId=9923;		
XN [1]		
FP SEQUENCE FROM N.A.		

```
RC TISSUE:Spleen;
RL Uemishi H.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
(12)
RA SEQUENCE OF 45-227 FROM N.A.
RL Han X., Tuch B.E.;
RA Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC - FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC - SUBUNIT: Homotrimer (By similarity).
CC - SUPRACELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC - PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC - SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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CC or send an email to license@isdb-sib.ch).
CC
CC EMBL; AB040443; BAB86593.1; -
DR EMBL; AF263915; AAK58524.1; -
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD00212; TNF_abc; 1.
DR ProDom; PD008002; TNF_5; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KM Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT
FT CHAIN 113 261
FT
FT FT DOMAIN 1 22
FT TRANSSEM 23 43
FT
FT DOMAIN 44 240
FT SITE 112 113
FT DISULFD 178 218
FT CARBOHD 240 240
SQ SEQUENCE 261 AA; 28869 MW; 28869 MM; 970007733455697 CRC64;

Query Match 86.1%; Score 1150; DB 1; Length 261;
Best Local Similarity 85.8%; Pred. No. 1,le-91;
Matches 224; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

OY 1 MIETYNQTSRPSAATGLPISMKI FMYLLTVFLITOMIGSLFAVYLHRRLDKIEDERNIA 60
Db 1 MIETYSQPSPRSVAAPBPVSMKIFMYLLTVFLITQMIGSLFAVYLHRRLDKIEDERNIH 60
OY 61 EDPEFMKTORTCMTGRGSRSLINLCSEIKSGQFEFVVDIMLNKEETKGNSPFEMQGDONP 120
Db 61 EDPEFKTTORTCKQGSGSLSLNCEIRSQFEDLVGMOSKEVKKKESPFMHMGDDOP 120
OY 121 QIAAHVISEASSTKTSVLQMAEKGYTYMMNNIVLTLENGKQLTVKRQGLYYIYAQTPCSN 180
Db 121 QIAAHVISEASSSTKTSVLQMAPRGYTTLSTNLVTLENGQLNVKGGIYYIYAQVTPCSN 180
OY 181 REASSQAPPFLASICTLKSPGFERILLRANTSHSAKPCCGQSIIHGAFELDPGASVPVN 240
Db 181 RDAAGQAPPFLASICTLRSPGSERIILLRANTSSSKPCGQSIIHGAFELDPGASVPVN 240
OY 241 VTDPSOVSHGTGTFSGTLKL 261
Db 241 VTDPSOVSHGTGTFSGTLKL 261
```

ID	TNFS_FELCA	STANDARD;	PRT;	260 AA.
GN	TNFSF5 OR CD40LG OR CD40L.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
NCBI	TaxID=9685;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thymus;			
RA	Hosie M.J., Willett B.J.;			
RT	"Adjuvant properties of feline CD154 (CD40 ligand).";			
RL	Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell			
CC	proliferation in the absence of co-stimulus as well as IGE			
CC	production in the presence of IL-4. Involved in immunoglobulin			
CC	class switching (By similarity).			
CC	- SUBUNIT: HOMODIMER. (By similarity).			
CC	- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN			
CC	EXTRACELLULAR SOLUBLE FORM (By similarity).			
CC	- PTM: The soluble form derives from the membrane form by			
CC	proteolytic processing (By similarity).			
CC	- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AF079105; AAD02954.1; -			
DR	HSSP; P29965; IALY.			
DR	InterPro; IPR003263; TNF_5.			
DR	InterPro; IPR003636; TNF_abc.			
DR	InterPro; IPR000478; TNF_family.			
DR	Pfam; PF00229; TNF; 1.			
DR	PfDom; PF008600; TNF_5; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS0049; TNF_2; 1.			
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.			
FT	CHAIN 1 260			
FT	TUMOR NECROSIS FACTOR LGAND SUPERFAMILY			
FT	MEMBER 5, MEMBRANE FORM.			
FT	TUMOR NECROSIS FACTOR LGAND SUPERFAMILY			
FT	MEMBER 5, SOLUBLE FORM (By similarity).			
FT	CYTOSOLSMIC (POTENTIAL).			
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)			
FT	(POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	CLEAVAGE (By similarity).			
FT	POTENTIAL.			
FT	N-LINKED (GLCNAC ...) (POTENTIAL).			
SO	SEQUENCE 260 AA; 28727 MW; 349FAD031EFB932 CRC64;			
Query Match	85.3%; Score 1138.5; DB 1; Length 260;			
Best Local Similarity	85.1%; Pred. No. 1e-90;			
Matches 222; Conservative 18; Mismatches 20; Indels 1; Gaps 1;				
0y	1 MIETNYOTSPSAAATG..DISIKIFMYLLTFLITQMGSAIFAVYLRRLDKIEDERH 60			
0b	1 MIETYSQAPBSVAGPVSMAKIFMYLLTFLITQMGSAIFAVYLRRLDKIEDERNY 60			

[illegible]

FT SITE 111 112 CLEAVAGE (BY SIMILARITY).  
 FT DISULFID 177 217 POTENTIAL.  
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 260 AA; 28688 MW; 604f69a19e98eb70 CRC64;

Query Match  
 Best Local Similarity 83.3%; Score 1112.5; DB 1; Length 260;  
 Matches 216; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 1 MIETNOTSPRRAATGLPISMKIFMYLLTVPLITOMISGALFAYVILHRDLKIEDERNH 60  
 DB 1 MIETNOTSPRRAATGLPISMKIFMYLLTVPLITOMISGALFAYVILHRDLKIEDERNH 60  
 QY 61 EDFVFMKTIOCRNCTGERSLILNCEBIKSOFEQFVNDIMLNKEETKENSFFMOKGDDNP 120  
 DB 61 EDFVFMKTIOCRNCTGERSLILNCEBIKSOFEQFVNDIMLNKEETKENSFFMOKGDDNP 119  
 QY 121 QIAAHVISEASSKTTSVLOMAEKGYTNMNNLVLTLENGKOLTVRKQGLYYIYAQVTPCSN 180  
 DB 120 QIAAHVISEASSKTTSVLOMAEKGYTNMNNLVLTLENGKOLTVRKQGLYYIYAQVTPCSN 179  
 QY 181 REASSQAFPIASLCLCKSPQRFERILLRANTHSSAKPCGQOSIHGVPFELQPGASVFN 240  
 DB 180 REASSQAFPIASLCLCKSPQRFERILLRANTHSSAKPCGQOSIHGVPFELQPGASVFN 239  
 QY 241 VTDPQVSHGTGFTSFGLKLT 261  
 DB 240 VTDPQVSHGTGFTSFGLKLT 260

## RESULT 10

TNFS\_MOUSE  
 ID TNFS\_MOUSE STANDARD; PRT; 260 AA.  
 AC P27548;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-  
 GN L) (TNF-related activation protein) (TRAF) (T cell antigen GP33).  
 GN TNFSF5 OR CD40LG OR CD40L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9224364; PubMed=1374165;  
 RA Armitage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L.,  
 RA Macduff B.M., Anderson D.M., Gimpel S.D., Davis-Smith T.,  
 RA Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,  
 RA Spriggs M.K.;  
 RT "Molecular and biological characterization of a murine ligand for  
 RT CD40.";  
 RL Nature 357:80-82(1992).  
 RP [2]  
 RP REVISION TO 198.  
 RA Spriggs M.K.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RP [3]  
 RP SEQUENCE OF 1-52 AND 137-260 FROM N.A.  
 RC STRAIN=129/Sv; TISSUE=Liver;  
 RX MEDLINE=94344153; PubMed=7520529;  
 RA Tsileikova E.N., Ramesh N., Geha R.S.;  
 RT "Structure of the murine CD40 ligand gene.";  
 RL Mol. Immunol. 31:895-900(1994).  
 RP [4]  
 RP SIMILARITY TO THE TNF FAMILY.  
 RX MEDLINE=92310561; PubMed=1377364;  
 RA Farrah T., Smith C.A.;  
 RT "Emerging cytokine family.";  
 RL Nature 358:26-26(1992).  
 RP [5]  
 RP 3D-STRUCTURE MODELING OF 115-260.

RX MEDLINE=93200072; PubMed=8095800;  
 RA Peitsch M.C., Jongeneel C.V.;  
 RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer  
 RT similar to the tumor necrosis factors.";  
 RL Int. Immunol. 5:233-236(1993)  
 CC -! FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell  
 CC proliferation in the absence of co-stimulus as well as Ige  
 CC production in the presence of IL-4. Involved in immunoglobulin  
 CC class switching (By similarity).  
 CC -! SUBUNIT: HOMOTRIMER.  
 CC -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -! TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+  
 CC T-LYMPHOCYTES.  
 CC -! PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -! SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X65453; CAA46448.2; -  
 CC EMBL; S71858; AAC13639.1; -  
 CC EMBL; S71861; AAC13640.1; -  
 CC PIR; S21738; S21738.  
 CC PDB; 1CDA; 31-OCT-93.  
 CC MGD; MGI:88337; Tnf5f5.  
 CC InterPro; IPR003263; TNF\_5.  
 CC InterPro; IPR003636; TNF\_abc.  
 CC InterPro; IPR004478; TNF\_family.  
 CC Pfam; PF00229; TNF\_1.  
 CC Prodom; PD008600; TNF\_5; 1.  
 CC SMART; SM00207; TNF; 1.  
 CC PROSITE; PS00251; TNF\_1; 1.  
 CC PROSITE; PS50049; TNF\_2; 1.  
 CC KMW; Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.  
 FT CHAIN 1 260  
 FT CHAIN 112 260  
 FT DOMAIN 1 22  
 FT TRANSMEM 23 46  
 FT DOMAIN 47 260  
 FT DISULFID 177 217  
 FT CARBOHYD 239 239  
 FT CONFLICT 198 198  
 SQ SEQUENCE 260 AA; 29370 MW; 7e1ac117473672ad CRC64;

Query Match  
 Best Local Similarity 77.3%; Score 1031.5; DB 1; Length 260;  
 Matches 202; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 1 MIETNOTSPRRAATGLPISMKIFMYLLTVPLITOMISGALFAYVILHRDLKIEDERNH 60  
 DB 1 MIETNOTSPRRAATGLPISMKIFMYLLTVPLITOMISGALFAYVILHRDLKIEDERNH 60  
 QY 61 EDFVFMKTIOCRNCTGERSLILNCEBIKSOFEQFVNDIMLNKEETKENSFFMOKGDDNP 120  
 DB 61 EDFVFMKTIOCRNCTGERSLILNCEBIKSOFEQFVNDIMLNKEETKENSFFMOKGDDNP 119  
 QY 121 QIAAHVISEASSKTTSVLOMAEKGYTNMNNLVLTLENGKOLTVRKQGLYYIYAQVTPCSN 180  
 DB 120 QIAAHVISEASSKTTSVLOMAEKGYTNMNNLVLTLENGKOLTVRKQGLYYIYAQVTPCSN 179  
 QY 181 REASSQAFPIASLCLCKSPQRFERILLRANTHSSAKPCGQOSIHGVPFELQPGASVFN 240

Db 180 REFSORPPIVGLMKRSGSERILLKQANTHSSSQLCEQSVHLGVFELQAGASVFN 239

Qy 241 VTDPSCVSHGTFSTFLKLT 261

Db 240 VTEASQVHHRVGFSSFGLLKLT 260

RESULT 11

TNFS RAT STANDARD; PRT; 260 AA.

AC 092372: 09R254: 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-

DE L).

GN TNFSF5 OR CD40LG OR CD40L.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Splenocyte;

RX MEDLINE=20284949; PubMed=10826698;

RA Hallett K.M., Oaks M.K.;

RT "Nucleotide sequence of the rat CD40 ligand.";

RL DNA Seq. 10:405-406(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=PVG; TISSUE=Spleen;

RA Daniel K.C., Foss Y., Mousavi A., Macary P., Kemeny D.M.,

RA Farzaneh F., Gaken J.A.;

RT "Cloning and sequencing of rat CD40 ligand.";

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

CC -i- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

CC -i- SUBUNIT: Homotrimer (By similarity).

CC -i- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

CC -i- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -i- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL; AF116582; AAD22460.1; -

DR EMBL; AF013985; AAD09323.1; -

DR HSSP; P27548; ICDA.

DR InterPro; IPR003263; TNF 5.

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR00478; TNF\_family.

DR Pfam; PF00229; TNF\_1.

DR ProDom; PD002012; TNF\_abc; 1.

DR ProDom; PD006600; TNF\_5; 1.

DR SMART; SM00207; TNF\_1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

FT CHAIN 1 260

FT CHAIN 112 260

FT DOMAIN 1 22

FT TRANSMEM 23 43

MEMBER 5. MEMBRANE FORM.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

MEMBER 5, SOLUBLE FORM (BY SIMILARITY).

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 44 260 (POTENTIAL).

FT SITE 111 112 EXTRACELLULAR (POTENTIAL).

FT DISULFID 177 217 CLEAVAGE (BY SIMILARITY).

FT CARBOHYD 239 239 POTENTIAL.

FT CONFLICT 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 114 114 P -> L (IN REF. 1).

FT CONFLICT 255 255 R -> K (IN REF. 1).

FT CONFLICT 255 255 I -> F (IN REF. 1).

SQ SEQUENCE 260 AA; 29259 MM; B303757D60D873A CRC64;

Query Match 76.4%; Score 1020.5; DB 1; Length 260;

Best Local Similarity 77.0%; Pred. No. 1.4e-80;

Matches 201; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

Qy 1 MIETYNQSPRSAAATGPIISKIFMYLLTVFLITQMIGSALFAYVLRRLKIDERNILH 60

Db 1 MIETYSQSPRSVATGLPASKMKIFMYLLTVFLITQMISVFPAYVLRRLKVEEASLH 60

Qy 61 EDFVFMKTQKCNTERSLSTLNCEIYSQTEGPKYDMLNKEETKENSFTMGQGNP 120

Db 61 EDFVFMKTLKRCNKGESLSLNCEMKRQEDLVKDISLNKEE-KKEKSEFMQRGDDP 119

Qy 121 OIAAHVISEASSKTSVYQMAEKGYTMSNNLVTLENGKOLTVRQGLYYIYAQVTFPSN 180

Db 120 OIAAHVSEANSNAASVLYQMAKKGYITKSNLVYLENGRQLTVRQGLYYIYQVTFPSN 179

Qy 181 REASSQAPFIASLCLKSPGFERILLRAANTHSSAKPGQOOSIHGCVFELQPGASVFN 240

Db 180 REPLSORPPIVSLWLMKPSGSERIILRAANTHSSSKLCEQSHHGCVFELQAGASVFN 239

Qy 241 VTDPSCVSHGTFSTFLKLT 261

Db 240 VTEASQVHHRVGFSSFGLLKLT 260

RESULT 12

TNFS CHICK STANDARD; PRT; 272 AA.

AC 0918D8;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-

DE L) (CD154 protein).

GN TNFSF5 OR CD40LG OR CD40L.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.

CC NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn; TISSUE=Spleen;

RA Tregaskes C.A., Young J.R., Burnside J.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -i- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

CC -i- SUBUNIT: Homotrimer (By similarity).

CC -i- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

CC -i- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -i- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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```

OY 66 MTIO-Q-RCWYGRSRSL-----NCEIISQEGFPKJDM-----LNKBTCK 107
Db 89 YHILRENTGLQDSTLSEEDTALPDSCKRMQAQGAQVRELQHI VGFQRFSPVPAM 148
OY 108 ENSF--EMQKGDPQIAAHVISEAS-----SKTTSVLQW-AEKGYTMSNNLVLTENGK 159
Db 149 EGSMTLDVARGRKEADQPAHLRTFNADIPSGSHKVSLSWYHGRMAKSN--MTLSNGK 206
OY 160 QLTWRQGLYYIAQVTPCSNPEASQAP-----FASLCLKSGRRERILPRAANT 211
Db 207 -LRVQDGGYYIYIANCF-RHHTSGASVPADYQLMYYVVKTSIKLPSHN--IMKGGST 262
OY 212 H--SSAKPCGQDSIHLGVFELOPGASVFENVTPDPSQVSHGTFSGTLKL 261
Db 263 KMSGNSSEHFHFSINVGFFKLARGESISQVSNPILDDQDQATYFGAKV 314

RESULT 14
TN11_MOUSE
ID TN11_MOUSE STANDARD; PRT; 316 AA.
AC 035235; 035306; Q9RIY0; Q9JUK8; Q9JUK9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-0UN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCS) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
DE (OCIF)
CN TNPSF11 OR RANKL OR TRANCE OR OPL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayan E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCS is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymic lymphoma;
RX MEDLINE=96032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
RA Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-C-cell function.";
RL Nature 390:175-179(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow stroma;
RX MEDLINE=98188248; PubMed=9520411;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA Motinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;

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RT "osteoclast differentiation factor is a ligand for  
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
RT to TRANCE/RANKL.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
RN [5]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP STRAIN=129;  
RC MEDLINE=99214075; PubMed=10196481;  
RX MEDLINE=99214075; PubMed=10196481;  
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
RA Ueda M., Higashio K.?  
RT "Cloning and characterization of the gene encoding mouse osteoclast  
RT differentiation factor."?  
RL Gene 230:121-127(1999).  
RN [6]  
RN SEQUENCE FROM N.A. (ISOFORMS 1: 2 AND 3).  
RP MEDLINE=21150053; PubMed=11250921.  
RX Ikeda T., Kasai M., Utsuyama M., Hirokawa K.?  
RA "Determination of three isoforms of the receptor activator of nuclear  
RT factor-kappaB ligand and their differential expression in bone and  
RT thymus."?  
RL Endocrinology 142:1419-1426(2001).  
RN [7]  
RN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.  
RP PubMed=10224132;  
RX Lam U., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,  
RA Schlegendorff J., Tempst P., Choi Y., Blobel C.P.?  
RT "Evidence for a role of a tumor necrosis factor-alpha  
RT (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a  
RT TNF family member involved in osteoclastogenesis and dendritic cell  
RT survival."?  
RL J. Biol. Chem. 274:13613-13618(1999).  
RN [8]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
RP PubMed=11581298;  
RX Lam U., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.?  
RA "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
RT of receptor-ligand specificity."?  
RL J. Clin. Invest. 108:971-979(2001).  
RN [9]  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
RP PubMed=11733492;  
RX Ito S., Wakabayashi K., Ushikata O., Hayashi S., Okada F., Hata T.?  
RA "Crystal structure of the extracellular domain of mouse RANK ligand at  
RT 2.2-A resolution."?  
RL J. Biol. Chem. 277:6631-6636(2002).  
RN [10]  
RN FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor  
CC augments the ability of dendritic cells to stimulate naive T-cell  
CC proliferation. May be an important regulator of interactions  
CC between T cells and dendritic cells and may play a role in the  
CC regulation of the T cell-dependent immune response. May also play  
CC an important role in enhanced bone-resorption in humoral  
CC hypercalcemia of malignancy.  
RN [11]  
RN SUBUNIT: Homotrimer.  
RN [12]  
RN SUBCELLULAR LOCATION: Type II membrane protein and secreted  
CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
RN [13]  
RN ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are  
CC produced by alternative splicing.  
RN [14]  
RN TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT  
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS  
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE  
CC TRABECULAR BONE AND LUNG.  
RN [15]  
RN PTM: N-glycosylated.  
RN [16]  
RN PTM: The soluble form of isoform 1 derives from the membrane form  
CC by proteolytic processing. The cleavage may be catalyzed by  
CC ADAM17. A further shorter soluble form was observed.  
RN [17]  
RN DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBULO-  
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH  
CC OF NEONORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPEOROSIS, WITH  
CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT  
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING  
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,  
CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN

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CC HYPERTROPHIC CHONDROCYTES.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF013170; AAC71061.1; -
DR EMBL: AF019048; AAB86812.1; -
DR EMBL: AF053713; AAC40113.1; -
DR EMBL: AB008426; BAA25425.1; -
DR EMBL: AB022039; BAA36970.1; -
DR EMBL: AB022036; BAA36970.1; JOINED.
DR EMBL: AB022037; BAA36970.1; JOINED.
DR EMBL: AB022038; BAA36970.1; JOINED.
DR EMBL: AB032771; BAA97257.1; -
DR EMBL: AB032772; BAA97258.1; -
DR EMBL: AB036798; BAA97259.1; -
DR PDB: 1J72; 12-SEP-01.
DR PDB: 1JQA; 13-MAR-02.
DR MGD; MGI:1100089; Tnfse11.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00228; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KM Cytochrome; Differentiation; Receptor; Glycoprotein; Transmembrane;
KM Signal-anchor; 3D-structure; Alternative splicing;
FT CHAIN 1 316
FT
FT CHAIN 139 316
FT
FT DOMAIN 1 48
FT TRANSMEM 49 69
FT
FT DOMAIN 70 316
FT SITE 138 139
FT CARBOHYD 197 197
FT CARBOHYD 262 262
FT VARSPIC 1 117
FT VARSPIC 14 44
FT
FT CONFLICT 99 99
FT CONFLICT 141 143
SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

Query Match 12.8% Score 171.5; DB 1; Length 316;
Best Local Similarity 25.2%; Pred. No. 1.7e-07;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

9 SPSSAAQLP--ISMKIFMYLLTFLITOMIGALFAVYLRHLD--KIEDER----- 57
33 APSAPAPAPPAARSMSFLALIGLGQVCSILF--LYPAQMDPRISDSHCHYRI 91
58 -NLHEDVFMKTIORCUTGERSLSL-----NCEIKSQEFGV-KDIW-----LN 101
92 LRLHE-----NAGLQDSLTSEBDTLPSDCRMKQAFQCAVQKEIQLHIYQPF 140
102 KEETKKEKNSF--EMQKQDNQPIAAHV-----ISEASSKTSYTLQNAEKGYTMSNNLV 153
141 GAPAMMGSWLDVQORKEPAQPAHLITNAASIPSGSHKVTLSWYHDKMAKISN--M 198
154 TLENGKQLYVRQGLYYIYAQVTFCSNRKASSQAP-----FIASICLKSPGRFRITL 205
199 TISNGK-LRVQDQDFYLYANICF-RHHEISGVPTDYLQLMVYVVKTSIKIPSSHN--L 254
206 LRAANTH--SSAKKCGGOSIHLGVPFELQPCASVFVAWVTPDSQVSHGTGFRISGLTL 261

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Db 255 MKGSTKNMGSSEFFHFYSINVGFPKLRAGEISIQVNSPLDPPQDATYFGAFKV 312

RESULT 15
TN11_HUMAN STANDARD; PRT; 317 AA.
AC 014788; 014723; 09P203; 096017;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCF) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
GN TNFSF11 OR RANKL OR TRANCF OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow, and Peripheral blood;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lymph node;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=9746112; PubMed=9312132;
RA Wong B.R., Rho J., Aron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCF is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Tongue;
RX MEDLINE=20175237; PubMed=10708588;
RA Nagai M., Kyakumoto S., Sato N.;
RT "Cancer cells responsible for humoral hypercalcemia express mRNA
RT encoding a secreted form of ODF/TRANCF that induces osteoclast
RT formation.";
RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1B/OPG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.

```

CC -1- SUBUNIT: Homotrimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);  
CC secreted (isoform 2). A soluble form of isoform 1 arises by  
CC proteolytic processing (By similarity).  
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;  
CC are produced by alternative splicing.  
CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT  
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,  
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.  
CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.  
CC -1- PTM: The soluble form of isoform 1 derives from the membrane form  
CC by proteolytic processing (By similarity). The cleavage may be  
CC catalyzed by ADAM17.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC -----  
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CC -----  
CC EMBL; AF019047; AAB6811.1; -;  
CC EMBL; AF053712; AAC39731.1; -;  
CC EMBL; AB064269; BAB79694.1; -;  
CC EMBL; AB061227; BAB71768.1; -;  
CC EMBL; AB064270; BAB79695.1; -;  
CC EMBL; AF013171; AAC51762.1; -;  
CC EMBL; AB037599; BAA90488.1; -;  
CC HSSP; P50591; IDOG.  
CC GeneW; HGNC:11926; TNFSF11.  
CC MIM; 602642; -;  
CC InterPro; IPR003636; TNF\_abc.  
CC InterPro; IPR000478; TNF\_family.  
CC Pfam; PF00229; TNF; 1.  
CC ProDom; PD002012; TNF\_abc; 1.  
CC SMART; SM00207; TNF; 1.  
CC PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
CC DR PROSITE; PS00049; TNF\_2; 1.  
CC KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
CC Signal-anchor; Alternative splicing.  
CC CHAIN 1 317  
CC FT CHAIN 140 317  
CC FT DOMAIN 1 47  
CC FT TRANSMEM 48 68  
CC FT DOMAIN 69 317  
CC FT SITE 139 140  
CC FT CARBOHYD 171 171  
CC FT CARBOHYD 198 198  
CC FT VARSPLIC 1 47  
CC FT VARSPLIC 1 73  
CC FT CONFLICT 194 194  
CC SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;  
Query Match 11.9%; Score 158.5; DB 1; Length 317;  
Best Local Similarity 24.5%; Pred. No. 2.2e-06;  
Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

Qy 174 QVTFCNSREASSQAP-----FIASCLKSPGFPERILLRAANTH--SSAKPGCGQSGIH 224  
Db 219 NICEFHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWGSNSERHFYSIN 276  
Qy 225 LGGVFELQPGASVFVNTDPSOVSHGTGFTSPGLKL 261  
Db 277 VGGFFKLRSGEISIEVSNPSLDDPDODATYFGAFKV 313

Search completed: June 7, 2003, 11:56:53  
Job time : 17.3518 secs

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OM protein - protein search, using sw model

Run on: June 7, 2003, 12:31:46 ; Search time 32 Seconds  
(without alignments)  
1680.572 Million cell updates/sec

Title: US-09-579-548a-1  
Perfect score: 1335  
Sequence: 1 MEITYNQTSPPRSATGATGLPIS.....TDPQVSHGTGFTSLTL 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	10.5	214	13 Q9DDZ5	Q9ddz5 brachydanio
2	135.5	10.1	215	11 Q99ND1	Q99nd1 lamiasciuru
3	129	9.7	214	6 Q9TTJ3	Q9ttj3 equus caball
4	126	9.4	217	6 Q9BEC5	Q9bec5 tenrec ecau
5	125	9.4	232	4 Q9UIV3	Q9uiv3 homo sapien
6	122	9.1	149	6 Q9T538	Q9t538 accus vocif
7	122	9.1	149	6 Q9TTG8	Q9ttg8 accus vocif
8	121	9.1	157	4 Q43647	Q43647 homo sapien
9	120.5	9.0	138	6 Q9TTG7	Q9ttg7 accus lemuri
10	118.5	8.9	287	13 Q90WT9	Q90wt9 gallus galli
11	118	8.8	149	6 Q9T543	Q9t543 accus nancy
12	113.5	8.5	216	6 Q9BEC4	Q9bec4 talpa europ
13	113	8.5	216	6 Q9BEE0	Q9bee0 macropus ru
14	112.5	8.4	156	11 Q91ZL4	Q91zl4 sigmodon hi
15	112.5	8.4	215	6 Q9BEE8	Q9bee8 erinaceus e
16	109.5	8.2	217	6 Q9BEG1	Q9beg1 bradypus tr

17	109	8.2	214	6 Q9BEE3	Q9bee3 didelphis m
18	108.5	8.1	217	6 Q9BEE4	Q9bee4 cabassous u
19	108.5	8.1	235	11 Q9J127	Q9j127 ratius norv
20	108.5	8.1	235	11 Q9J126	Q9j126 ratius norv
21	108.5	8.1	649	10 Q9M549	Q9m549 cucumis sat
22	107	8.0	216	6 Q9BEC9	Q9bec9 ochotona pr
23	106.5	8.0	217	6 Q9BEG0	Q9beg0 cyclopes di
24	106	7.9	217	11 Q9BEG6	Q9beg6 peromyscus
25	103.5	7.8	255	13 Q91810	Q91810 salvelinus
26	99.5	7.5	246	13 Q91976	Q91976 oncorhynch
27	99.5	7.5	246	13 Q91970	Q91970 oncorhynch
28	99	7.4	1193	4 Q92580	Q92580 homo sapien
29	98.5	7.4	225	13 Q91B42	Q91b42 paralichth
30	97.5	7.3	255	13 Q9DEP9	Q9dep9 oncorhynch
31	97.5	7.3	1217	10 Q9SRY2	Q9sry2 aradidopsis
32	95.5	7.2	1817	5 Q96206	Q96206 plasmodium
33	95.5	7.2	2166	16 Q51465	Q51465 borrelia bu
34	94.5	7.1	706	2 Q85052	Q85052 moraxella c
35	93.5	7.0	225	13 Q91B41	Q91b41 paralichth
36	93	7.0	169	11 Q9WV90	Q9wv90 marmota mon
37	93	7.0	216	11 Q70332	Q70332 mesocricetu
38	93	7.0	582	16 Q97E09	Q97e09 clostridium
39	93	7.0	822	16 Q8YKQ9	Q8ykq9 anabaena sp
40	92	6.9	773	10 Q8W0K4	Q8w0k4 oryza sativ
41	91.5	6.9	1864	10 Q9FYL7	Q9fy17 arabidopsis
42	89.5	6.7	463	2 Q9KH42	Q9kh42 clostridium
43	88.5	6.6	401	5 Q27229	Q27229 dictyosteli
44	88.5	6.6	1819	16 Q97K40	Q97k40 clostridium
45	88	6.6	418	17 Q8TM51	Q8tm51 methanobarc

ALIGNMENTS

RESULT 1  
Q9DDZ5 PRELIMINARY: PRT: 214 AA.  
AC Q9DDZ5;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
DE TRAIL-1-like protein.  
GN TNFSF10L.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bobe J., Goetz F.W.;  
RT "Molecular cloning and expression of a TNF receptor and two TNF  
RT ligands in the fish ovary".  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
DR EMBL: AF250041; AAG47640.1; --  
DR HSP; P50591; IDOG.  
DR ZFIN: ZDB-GENE-010801-1; tnfsf10l.  
DR InterPro: IPR003636; TNF abc.  
DR InterPro: IPR00478; TNF\_family.  
DR Pfam: PF00229; TNF; 1.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; P550049; TNF\_2; 1.  
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;  
Query Match 10.5%; Score 140; DB 13; Length 214;  
Best Local Similarity 25.5%; Pred. No. 0.00059;  
Matches 60; Conservative 30; Mismatches 95; Indels 50; Gaps 9;  
QY 45 YLHRLDKIEDERNLH-----EDFVFMKTIORCNTGERSISLNLNCEIKSQFG 93  
DB 10 YISKVTDELISKOTLHAARTOTHSYNTGSKMTTVMORPSAHLTUS----- 56

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QY 94 FVKDMLNKEETKENSEFEMQKQDQNPQIAAHVISEASKTTSVLOWAEKGYTMSNNLV 153
DB 57 -----SASBDS- RPOSDMHQPOFDLH-----QSCRHPVHTAMCSFGALHYM- 98
QY 154 TLNGKQLTVKROGLYYIYAQVTF-----CSNREASSQAPFIASLCLSPGFEEL-LLRA 208
DB 99 TLITNGR-LRYPQDGRYTLISQVYFRYRPSPSDSSSHQVQVCITYKTSYLNPIQLKKG 157

QY 209 ANTHSSAKPC--GOOSIHLGVEFLOPGASVFNVTTPSQVSHGTGFTSPGLKL 261
DB 158 VGRICWAPDAEYALHSHVYQGLFELRAGDEVFVSVSPTWYGGEDSSSYFCAPRL 212

RESULT 2
Q99ND1 PRELIMINARY; PRT; 215 AA.
ID 099ND1
AC 099ND1
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tamiasciurus hudsonicus (American red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamiasciurus.
OX NCBI_TaxId=10009;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ286824; CAC28540.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match 10.1%; Score 135.5; DB 11; Length 215;
Best Local Similarity 29.6%; Pred. No. 0.0014;
Matches 55; Conservative 27; Mismatches 63; Indels 41; Gaps 9;

QY 81 LLNCEERKSQFEGFVKDMLNKEE---TKENSEFEMQKQDQNPQIAAHVISEASKTTSV 137
DB 41 LHHGVIIGPREPFPNNLPLSAQOMLTRSSQNM-----NDKPVAVHV---ANQIBEQ 92
QY 138 LOW-AEKGYYTMSNNLVTLNGKQLTVKROGLYYIYAQVTF-----CSNREASSQAPFIAS 192
DB 93 LOWLSRANMLLANGMELIDN--QLVVPADLYLISQVLFKGGCGSS-----YV 140
QY 193 LCKSPGFRFERILLRANNTSSAK-PCGQOS-----THLGVEFLOPGASVFN 239
DB 141 LHTTVSRFAVSVDKYNLISAKSPCKESLBGAEPKWPYEPYLYLGVEFLOKGRISA 200

QY 240 NVTDPSS 245
DB 201 EVNLPSS 206

RESULT 3
Q99TJ3 PRELIMINARY; PRT; 234 AA.
ID 099TJ3
AC 099TJ3
DT 01-MAY-2000 (TREMBlrel. 13, Created)

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DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor-alpha.
GN TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=THOROUGHRED, TISSUE=ARTERIAL ENDOTHELIUM;
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB035735; BAA88349.1; -.
DR HSSP; P01375; 1A8M.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 234 AA; 25430 MW; 2384D950A21F377 CRC64;

Query Match 9.7%; Score 129; DB 6; Length 234;
Best Local Similarity 27.9%; Pred. No. 0.0055;
Matches 51; Conservative 33; Mismatches 69; Indels 30; Gaps 11;

QY 102 KEETKENSEF-----MOKQDNP-QIAAHVISEASKTTSVLOW-AEKGYTMSN 150
DB 59 QREQLNARQSIINPLAQTLRSSSRTPSDKPVAVHV--ANQOAGOLQMSGRANALLAN 116
QY 151 NLYTLNGKQLTVKROGLYYIYAQVTFCSNREASSQAPF---IASLCKSPGFRERILLR 207
DB 117 GVKLTDN--QLVVPDLGLYLSQVLFKGGCGPSTHYLLHTTISRLAVSYSKVN--LLS 172
QY 208 A---ANTHS---SAPPCGQOSIHLGVEFLOPGASVFNVTTPSQVSHG-TGFTSPGL 258
DB 173 AIKSLANTEPEQAEAPR-WPEPIYLGVEFLEKGDQLSAEINQPNYLDFAESQGVYRG 231
QY 259 LKL 261
DB 232 IAL 234

RESULT 4
Q99BC5 PRELIMINARY; PRT; 217 AA.
ID 099BC5
AC 099BC5
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tenrec ecaudatus (tailless tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.
OX NCBI_TaxId=94439;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ286826; CAC28538.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.

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DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS0049; TNF\_2; 1.  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 217 AA; 23845 MW; 1C5013E9B777B54A CRC64;  
  
Query Match 9.4%; Score 126; DB 6; Length 217;  
Best local Similarity 22.8%; Pred. No. 0.0089;  
Matches 61; Conservative 33; Mismatches 90; Indels 82; Gaps 11;  
  
QY 2 IETVNOTSPRSAAATGUP-----ISMKIFMYLLTVLLITOMIGSALFAVILHRLDKIED 55  
DB 1 VELAEETLPKPK--SGAPQGSRRCLCLSLFSLF-----VAGATLLFCLLHGVIGPQR 51  
QY 56 ERRLHEDFVPMKTI-QRCNTGERSLSLNEEETKSQEPGVKQIMLNKEETKENSFEMQ 114  
DB 52 EEOFPSSPHLIKPLTQRLRSSKRLS----- 77  
QY 115 KGDQNPQIAAHVISEASSKTTSVLOWAEK-GYYTMSNNLVLENGKQLTWKQGLYYIYA 173  
DB 78 -----DKPAHVH--ASTQDEGQLKWVKSKANMLDNNVQILDN--QLVPLDGLYIYIS 128  
QY 174 QVTF-----CSNEPSSQAPFIASLCLKSPRRERILLRANTHSSAKPC 218  
DB 129 QVLFKGPQGHGTIVYLTHTVSRIVASVQAKVNLISAKTPCH-----RTPGGSSEKPF 181  
QY 219 GQGSIHLLGGVFELOPGASVFNVTDPDS 245  
DB 182 WTEPYLGGVFPQLQKGRUSAEINLPN 208  
  
RESULT 5  
OSU1V3 PRELIMINARY; PRT; 232 AA.  
AC 09U1V3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Tumor necrosis factor.  
GN TNF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93272029; PubMed=8499947;  
RA Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,  
RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;  
RT "Dense Alu clustering and a potential new member of the NkappaB  
RT family within a 90 kilobase HLA class III segment.";  
RL Nat. Genet. 3:137-145(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96215741; PubMed=8629302;  
RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,  
RA Wallace A.F., Russell M.E.;  
RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage  
RT molecule expressed in transplanted human hearts.";  
RL Transplantation 61:1387-1392(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96006565; PubMed=7590964;  
RA Holinger I., de Baey A., Messer G., Kick G., Zietzina H.,  
RA Weiss E.H.;  
RT "Cloning and genomic characterization of LST1: a new gene in the human  
RT TNF region.";  
RL Immunogenetics 42:315-322(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93208881; PubMed=7916655;  
RA Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,

RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;  
RT "Lymphotixin-beta: A new member of the TNF family that forms a  
RT heteromeric complex with lymphotxin on the cell surface.";  
RL Cell 72:847-856(1993).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86016093; PubMed=2995927;  
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,  
RA Pennica D., Goeddel D.V., Gray P.W.;  
RT "Human lymphotxin and tumor necrosis factor genes: structure,  
RT homology and chromosomal localization.";  
RL Nucleic Acids Res. 13:6361-6373(1985).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91086846; PubMed=1670638;  
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,  
RA Rietmuller G., Weiss E.H.;  
RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An  
RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene  
RT Correlates with A Variant Amino Acid in Position 26 and a Reduced  
RT Level of TNF-beta Production.";  
RL J. Exp. Med. 173:209-219(1991).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139175; PubMed=1671667;  
RA Abraham I.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;  
RT "Haplotypic polymorphisms of the TNFB gene.";  
RL Immunogenetics 33:50-53(1991).  
RN [8]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94362679; PubMed=8081366;  
RA Albertella M.R., Campbell D.R.;  
RT "Characterization of a novel gene in the human major  
RT histocompatibility complex that encodes a potential new member of the  
RT I kappa B family of proteins.";  
RL Hum. Mol. Genet. 3:793-799(1994).  
RN [9]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95324911; PubMed=7601445;  
RA Peelman L., Charodon P., Nunes M., Renard C., Gelfrocin C., Vaiman M.,  
RA Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,  
RA Strominger J., Spies T.;  
RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative  
RT Nuclear RNA Helicase of the D-E-A-D Family.";  
RL Genomics 26:210-218(1995).  
RN [10]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20132445; PubMed=10668961;  
RA Neville M.J., Campbell R.D.;  
RT "Alternative splicing of the LST-1 gene located in the major  
RT histocompatibility complex on human chromosome 6.";  
RL DNA Seq. 8:155-160(1997).  
RN [11]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98035883; PubMed=9367684;  
RA de Baey A., Fellerhoff B., Maier S., Martinuzzi S., Weidle U.,  
RA Weiss E.H.;  
RT "Complex expression pattern of the TNF region gene LST1 through  
RT differential regulation, initiation, and alternative splicing.";  
RL Genomics 45:591-600(1997).  
RN [12]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98149985; PubMed=9480751;  
RA Shima T., Tamaya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,  
RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,  
RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,  
RA Kimura M., Inoko H.;  
RT "Nucleotide sequencing analysis of the 146-kilobase segment around the  
RT Ikbl and MICA genes at the centromeric end of the HLA class I  
RT region.";  
RL Genomics 47:372-382(1998).  
DR EMBL; Y14768; CAAV5070.1; -  
DR HSSP; P01375; 4TSV.







RT in 4 *Aotus* species";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL AF014513; AAD01539.1; -.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_\_abc.  
 DR InterPro: IPR000478; TNF\_\_family.  
 DR Pfam: PF00229; TNF: 1.  
 DR PRINTS: PR01234; TNFCROSISFCT.  
 DR Prodom: PD002012; TNF\_\_adc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 149  
 FT NON\_TER 149  
 SO SEQUENCE 149 AA; 1646 MW; 3C2A6140778EFA8A CRC64;

[illegible][illegible]

Query Match 8.5%; Score 113.5; DB 6; Length 216;  
Best local Similarity 33.1%; P-Id No.0.997;  
Matches 45; Conservative 17; Mismatches 49; Indels 25; Gaps 8;

124 AHVISAASSTTYSVLWAEKGYITMSNNLTLENGKQLYTKRGATYYIAQT-----C- 178  
||| ||||  
Db 81 AHHV--AANPDAGCOLMISOVANALLANGELTN-NQLVPSPGGLIYISOVFPEKGCGP 137

Qy	179	SN-----	REASQAFIASI-	CIKSPGFERLLR	LAANTHSSAKPCGQDS	IHUGV	228
Db	138	SNLVLTTHKIQTA	SYEDAVDLLSAIKS	PCO-----	RETPEGARP-	WYPIVLGV	190
Qy	229	PELOFGASYFN	VNTDP	244			
Db	191	FOLEKGDRISAN	INLP	206			

SQ	SEQUENCE	216 AA;	23829 MW;	3AF7E646B2D4AFED CRC64;
FT	NON_TER	1	1	
DR	PROSITE; PS50049;	TNF_2;	1.	
DR	PROSITE; PS00251;	TNF_1;	1.	
DR	SMART; SMO0207;	TNF_1.		
DR	Pfdom; PF002012;	TNF_abc;	1.	
DR	PRINTS; PR01234;	TNCRGROSISFCT.		
DR	Pfam; PF00229;	TNF_1		
DR	IInterPro; IPR003636;	TNF_abc.		
DR	HSSP; P01375;	ATSV.		
DR	EMBL; AJ286833;	CAC28527.1;	-.	
RL	Submitted (Feb-2000)	to the EMBL/GenBank/DBJ databases.		
RT	their sister group."			
RA	"Indices indicate that rodents are monophyletic and lagomorphs are			
RP	van Dijk M.A.M., de Jong W.W.;			
OC	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.			
OX	[1]_TaxID=9921;			
OS	Macropus rufus (Red kangaroo) (Megalasia rufa).			
OT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DE	Tumor necrosis factor (Fragment).			
DT	01-JUN-2001 (TREMBlrel. 17, last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
ID	Q9BEEO;	PRELIMINARY;	PRT;	216 AA.
AC	Q9BEEO;			
RE	01-JUN-2001 (TREMBlrel. 17, Created)			
RE	01-JUN-2001 (TREMBlrel. 17, last sequence update)			
RE	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
RE	Tumor necrosis factor (Fragment).			
RE	TNFA.			
RE	Macropus rufus (Red kangaroo) (Megalasia rufa).			
RE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RE	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.			
RE	[1]_TaxID=9921;			
RE	SEQUENCE FROM N.A.			

	Query Match	8.5%; Score 113; DB 6;	Length 216;
	Best Local Similarity	22.2%; Pred. No. 0.11;	
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			Gaps 11;
OY	27 LITVETLTOMIGSALFAVYLHRRLDKIEDERNLHEDEVFMK----	TIORCNTGERSISLL	82
Dd	25 ILTFPL--LAGATLFLCGLHPGVIGQNEESTDALGMKPVTQRVRSCT-----	74	
OY	83 NCEBIKSQEPGFVKVDIMLNKEETKKENSFEMOKDONDPOIAAHVISSEASKTTSVLQWAE	142	
Dd	75 -----ESNKP-----VAHVADPDLAE--GKLWLK	97	
OY	143 -KGYTMSNNLVTLENGSKQLTVRKGLYYTYAAOVTF-----CSNR-----EASSQ	186	
Dd	98 RRAVNVLINSGMDLYDN--QLVPSTGTGLYVSQLLFGEDCANBPILLTHTVSRVALSYQ	155	
OY	187 APTIASLCUKSPERFERILIRANHTSSNAFCGGQSIIHGCVELQGSASPVAVNTDPS	245	
Dd	156 SKYNLSAIKSPQ----KTIVGARREASP-WYEPIYGCVFQLREGDKTSLADTNYPN	207	
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ID	O91ZL4	PRELIMINARY;	PRT;    156 AA.
AC	O91ZL4;		
DT	01-DEC-2001 (TEMBLrel. 19, Created)		
DT	01-DEC-2001 (TEMBLrel. 19, Last sequence update)		
DT	01-MAR-2002 (TEMBLrel. 20, Last annotation update)		
S	Tumor necrosis factor alpha (Fragment).		
S	Stimodon hispidus (Hispid cotton rat).		



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OM protein - protein search, using sw model

Run on: June 7, 2003, 14:08:56 ; Search time 36 Seconds  
(without alignments)  
966.067 Million cell updates/sec

Title: US-09-579-548A-1  
Perfect score: 1335  
Sequence: 1 MIETNNGTSPRSANGLPIS.....TDPQVSHGTGTFSLKLK 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	261	14	CD40-L, Homo sapi
2	1335	100.0	261	15	CD40-L, Homo sapi
3	1335	100.0	261	15	CD40-L, Homo sapi
4	1335	100.0	261	15	CD40-L, Homo sapi
5	1335	100.0	261	15	CD40-L, Homo sapi
6	1335	100.0	261	15	CD40-L, Homo sapi
7	1335	100.0	261	15	CD40-L, Homo sapi
8	1335	100.0	261	15	CD40-L, Homo sapi
9	1335	100.0	261	15	CD40-L, Homo sapi
10	1335	100.0	261	15	CD40-L, Homo sapi

11	1335	100.0	261	22	AA67612	Amino acid sequenc
12	1335	100.0	261	23	AB808131	Human CD40L, poly
13	1335	100.0	261	23	AA49202	Human CD145, Homo
14	1335	100.0	261	23	AB805350	Human CD154, amino
15	1335	100.0	261	23	AB804674	Human CD40L, extrac
16	1335	100.0	261	22	AB82384	Novel human diagno
17	1335	100.0	261	18	AAW09122	CD40 ligand/zipper
18	1335	99.9	261	23	AA837806	Human CD40 ligand
19	1331	99.7	261	23	AAW49207	Human CD145 mutan
20	1331	99.7	261	23	AAW49213	Human CD145 mutan
21	1330	99.6	261	23	AAW49206	Human CD145 mutan
22	1330	99.6	261	23	AAW49208	Human CD145 mutan
23	1330	99.6	261	23	AAW49220	Human CD145 mutan
24	1330	99.6	261	23	AAW49224	Human CD145 mutan
25	1330	99.6	261	23	AAW49226	Human CD145 mutan
26	1330	99.6	261	18	AAW09119	CD40 ligand/zipper
27	1329	99.6	261	23	AAW49205	Human CD145 mutan
28	1329	99.6	261	23	AAW49211	Human CD145 mutan
29	1329	99.6	261	23	AAW49214	Human CD145 mutan
30	1329	99.6	261	23	AAW49219	Human CD145 mutan
31	1329	99.6	261	23	AAW49221	Human CD145 mutan
32	1329	99.6	261	23	AAW49222	Human CD145 mutan
33	1329	99.6	261	23	AAW49227	Human CD145 mutan
34	1329	99.6	261	23	AAW49229	Human CD145 mutan
35	1329	99.6	261	18	AAW09121	CD40 ligand/zipper
36	1328	99.5	261	23	AAW49210	Human CD145 mutan
37	1328	99.5	261	23	AAW49217	Human CD145 mutan
38	1327	99.4	261	23	AAW49215	Human CD145 mutan
39	1327	99.4	261	23	AAW49228	Human CD145 mutan
40	1326	99.3	261	23	AAW49216	Human CD145 mutan
41	1326	99.3	261	23	AAW49218	Human CD145 mutan
42	1326	99.3	261	23	AAW49223	Human CD145 mutan
43	1326	99.3	261	18	AAW09120	CD40 ligand/zipper
44	1325	99.3	261	18	AAW09114	Human CD40L, mutan
45	1325	99.3	261	23	AAW49225	Human CD145 mutan

#### ALIGNMENTS

RESULT 1	AA836701	standard; Protein; 261 AA.
ID	AA836701	
XX	AA836701;	
AC	AA836701;	
XX		
DT	12-AUG-1993	(first entry)
DE	CD40-L.	
XX		
KW	Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;	
KW	transmembrane; region; intracellular; soluble; activity; B cell;	
KW	proliferation; induction; antibody; secretion; IGE; agonist;	
KW	antagonist; binding assay.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	47..261
FT		/note="Extracellular region"
PN	MO9308207-A.	
PD	29-APR-1993.	
XX		
PF	23-OCT-1992;	92WO-US08990.
XX		
PR	25-OCT-1991;	91US-0783707.
PR	05-DEC-1991;	91US-0805723.
XX		
PA	(IMMUNEX CORP.	
XX		
PI	Armitage RJ, Fanslow WC, Spriggs MK;	

XX MPI: 1993-152417/18.  
 DR N-PSDB; AAQ41506.  
 XX New cytokine CD40-L as CD40 agonist and antagonist - is used for  
 PT treating allergies, lupus, rheumatoid arthritis,  
 PT graft-versus-host disease and insulin-dependent diabetes mellitus  
 XX Claim 1; Fig 2; 80pp; English.  
 PS  
 XX This sequence represents human CD40-L polypeptide which binds to CD40.  
 CC CD40-L is a type II membrane polypeptide which has an extracellular  
 CC region at its C-terminus, a transmembrane region and an  
 CC intracellular region at its N-terminus. A soluble form of CD40-L  
 CC lacks the transmembrane domain. CD40-L activity is mediated by  
 CC binding with CD40 an dinduces B cell proliferation and induction of  
 CC antibody secretion, including IgE. Membrane bound CD40-L acts as a  
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L  
 CC can be used in a binding assay to detect cells expressing CD40.  
 XX  
 SQ Sequence 261 AA;  
 Query Match 100.0%; Score 1335; DB 14; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MIETVNTSPRSATGLPISMKIFMYLLTVFLITOMIGSALFAYLHRRLDKIEDERNLH 60  
 Db 1 MIETVNTSPRSATGLPISMKIFMYLLTVFLITOMIGSALFAYLHRRLDKIEDERNLH 60  
 QY 61 EDVFMKTIORCNGERSLSLNCCEIKSQFEGFVKDIMNKETKENSFEWQKQDNP 120  
 Db 61 EDVFMKTIORCNGERSLSLNCCEIKSQFEGFVKDIMNKETKENSFEWQKQDNP 120  
 QY 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVLENGKQLTVRQGLYYIYAQVTCNS 180  
 Db 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVLENGKQLTVRQGLYYIYAQVTCNS 180  
 QY 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVFELQPGASVFN 240  
 Db 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVFELQPGASVFN 240  
 QY 241 VTDPSQVSHGTGFTSFGLKL 261  
 Db 241 VTDPSQVSHGTGFTSFGLKL 261  
 RESULT 2  
 AAR53969  
 ID AAR53969 standard; Protein; 261 AA.  
 XX  
 AC AAR53969;  
 XX  
 DT 11-JAN-1995 (first entry)  
 XX  
 DE Human CD40-L type II transmembrane protein.  
 XX  
 KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;  
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;  
 KW soluble CD40-L; tumour necrosis factor family.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 50..261  
 FT /label= "extracellular region  
 FT /note= "soluble CD40-L"  
 XX  
 PN MO9410308-A.  
 XX  
 PD 11-MAY-1994.  
 XX  
 PF 20-OCT-1993; 93WO-US10034.

XX  
 PR 23-OCT-1992; 92US-0969703.  
 PR 13-AUG-1993; 93US-0107353.  
 XX  
 PA (IMMUNEX ) IMMUNEX CORP.  
 PI Spriggs MK, Srinivasan S;  
 XX MPI: 1994-167465/20.  
 DR N-PSDB; AAR53969.  
 XX  
 PT Pregn. of soluble oligomeric mammalian proteins - using host  
 PT cells to express a fusion protein comprising a leucine zipper  
 PT domain and a heterologous mammalian protein  
 XX  
 PS Example 1; Page 24; 35pp; English.  
 CC  
 CC A DNA fragment encoding the extracellular (soluble) region of human  
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding  
 CC for a leader peptide, a 33 amino acid leucine zipper sequence  
 CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the  
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L  
 CC in the supernatant. The leucine zipper sequence spontaneously  
 CC trimerises in solution and fusion proteins comprising  
 CC the sequence fused to a heterologous mammalian protein also form  
 CC oligomers.  
 XX  
 SQ Sequence 261 AA;  
 Query Match 100.0%; Score 1335; DB 15; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MIETVNTSPRSATGLPISMKIFMYLLTVFLITOMIGSALFAYLHRRLDKIEDERNLH 60  
 Db 1 MIETVNTSPRSATGLPISMKIFMYLLTVFLITOMIGSALFAYLHRRLDKIEDERNLH 60  
 QY 61 EDVFMKTIORCNGERSLSLNCCEIKSQFEGFVKDIMNKETKENSFEWQKQDNP 120  
 Db 61 EDVFMKTIORCNGERSLSLNCCEIKSQFEGFVKDIMNKETKENSFEWQKQDNP 120  
 QY 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVLENGKQLTVRQGLYYIYAQVTCNS 180  
 Db 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVLENGKQLTVRQGLYYIYAQVTCNS 180  
 QY 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVFELQPGASVFN 240  
 Db 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVFELQPGASVFN 240  
 QY 241 VTDPSQVSHGTGFTSFGLKL 261  
 Db 241 VTDPSQVSHGTGFTSFGLKL 261  
 RESULT 3  
 AAR57469  
 ID AAR57469 standard; Protein; 261 AA.  
 XX  
 AC AAR57469;  
 XX  
 DT 23-MAR-1995 (first entry)  
 XX  
 DE CD40 ligand.  
 XX  
 KW Probe; primer; PCR; amplify; polymerase chain reaction; detection;  
 KW mutation; CD40 ligand gene; IgM; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN MO9417196-A.  
 XX  
 PD 04-AUG-1994.  
 XX

PF 21-JAN-1994; 94MO-US00786.  
 XX  
 PR 22-JAN-1993; 93US-0009258.  
 XX 20-JAN-1994; 94US-0184422.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;  
 PI Spriggs MK, Widmer MB;  
 XX  
 DR WPI: 1994-264109/32.  
 XX N-PSDB; AA067123.  
 XX  
 PT Method for detecting mutation in CD 40 ligand gene - comprises  
 XX amplification of nucleic acid, and mutational analysis  
 XX  
 PS Disclosure; Page 22-24; 38pp; English.  
 XX  
 CC This sequence is encoded by the CD40 ligand gene. Mutations within  
 CC the CD40 ligand gene were identified by the method of the invention.  
 CC The method comprises isolating DNA from an individual and selectively  
 CC amplifying the isolated DNA derived from the CD40 ligand gene. The  
 CC amplification product is then analysed to determine if there is a  
 CC mutation present and determining if a protein expressed from the  
 CC ligand gene will bind CD40. The detection of mutations in the CD40  
 CC ligand gene allows subsequent treatment of a syndrome resulting in  
 CC elevated levels of serum IgM and diminished levels of other Ig  
 CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked  
 CC hyperIgM syndrome.  
 XX  
 SQ Sequence 261 AA;  
 XX  
 Query Match 100.0%; Score 1335; DB 15; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLLTOMIGSALPAVYLHRRLDKIEDERNLH 60  
 Db 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLLTOMIGSALPAVYLHRRLDKIEDERNLH 60  
 QY 61 EDFVFMKTIQRNCTGERSLSLNCERIKSQFEGFVDMIMLNKEETKENSFEMQKGDNP 120  
 Db 61 EDFVFMKTIQRNCTGERSLSLNCERIKSQFEGFVDMIMLNKEETKENSFEMQKGDNP 120  
 QY 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVTLENGKOLTVKRGLYIYAQVTFCSN 180  
 Db 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVTLENGKOLTVKRGLYIYAQVTFCSN 180  
 QY 181 REASSQAPPIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVEFELPGASVFN 240  
 Db 181 REASSQAPPIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVEFELPGASVFN 240  
 QY 241 VTDPQOVSHGTGFTSFGLIKL 261  
 Db 241 VTDPQOVSHGTGFTSFGLIKL 261

## RESULT 4

AA085486  
 ID AA085486 standard; Protein; 261 AA.  
 XX  
 AC AA085486;  
 XX  
 DT 18-MAR-1996 (first entry)  
 XX  
 DB Human CD40 ligand.  
 XX  
 XX High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;  
 KM differentiation; proliferation; baculovirus; Spodoptera frugiperda;  
 XX Sf9; insect cell culture; tumour necrosis factor receptor.  
 XX  
 XX Homo sapiens.  
 XX

EH Key Location/Qualifiers  
 FT Modified-site 6.8  
 FT /label= N-glycosylation\_site  
 FT Domain 23..46  
 FT /label= Transmembrane\_domain  
 FT Modified-site 239..241  
 FT /label= N-glycosylation\_site  
 XX  
 PN W09529935-A1.  
 XX  
 PD 09-NOV-1995.  
 XX  
 PF 28-APR-1995; 95MO-US05448.  
 XX  
 PR 28-APR-1994; 94US-0234580.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
 XX  
 PI Castle BE, Kehnry M;  
 XX  
 DR WPI: 1995-393038/50.  
 XX N-PSDB; AAT05763.  
 XX  
 PT High density membrane bound CD40 ligand - for stimulating the  
 PT proliferation of B cells in vitro or in vivo, partic. for producing  
 PT differentiated cells  
 XX  
 PS Disclosure; Fig 1; 74pp; English.  
 XX  
 CC Human high-density, membrane-bound (hdmB) CD40 ligand (AA085486) is a  
 CC type 2 membrane glycoprotein expressed in activated T-cells. It is  
 CC a member of the tumour necrosis factor receptor family. hdmBCD40  
 CC induces long-term proliferation of B-cells in culture. These  
 CC proliferating B-cells can be induced to differentiate into antibody-  
 CC prodn. cells. Proliferation and differentiation in the presence of an  
 CC antigen preferentially proliferates or selects differentiating B-cells  
 CC to produce antibodies specific to that antigen. Recombinant hdmBCD40  
 CC is obtd. by incorporating encoding DNA (AAT05763) into a baculovirus  
 CC vector that is then used to transfect Sf9 insect cells.  
 XX  
 SQ Sequence 261 AA;  
 XX  
 Query Match 100.0%; Score 1335; DB 16; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLLTOMIGSALPAVYLHRRLDKIEDERNLH 60  
 Db 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLLTOMIGSALPAVYLHRRLDKIEDERNLH 60  
 QY 61 EDFVFMKTIQRNCTGERSLSLNCERIKSQFEGFVDMIMLNKEETKENSFEMQKGDNP 120  
 Db 61 EDFVFMKTIQRNCTGERSLSLNCERIKSQFEGFVDMIMLNKEETKENSFEMQKGDNP 120  
 QY 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVTLENGKOLTVKRGLYIYAQVTFCSN 180  
 Db 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVTLENGKOLTVKRGLYIYAQVTFCSN 180  
 QY 181 REASSQAPPIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVEFELPGASVFN 240  
 Db 181 REASSQAPPIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGVEFELPGASVFN 240  
 QY 241 VTDPQOVSHGTGFTSFGLIKL 261  
 Db 241 VTDPQOVSHGTGFTSFGLIKL 261

## RESULT 5

AA034669  
 ID AA034669 standard; Protein; 261 AA.  
 XX  
 AC AA034669;  
 XX

DT 16-FEB-1998 (first entry)

DE Amino acid sequence for CD40L, a novel cytokine ligand for CD40,  
xy

KM Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;  
 KW neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;  
 KW melanoma; carcinoma.

OS Homo sapiens

PN US5674492-A.

PD 07-OCT-1997.

PF 21-DEC-1994; 94US-0360923.

PR 23-DEC-1993; 93US-0172664.

PA (IMMV) IMMUNEX CORP.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 VV

PI Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;  
xy

DR WPI; 1997-502273/46.

DK N-PSDB; AA193782.  
XX

PT Treating or preventing neoplastic disease associated with CD40-expressing cells - particularly B-cell lymphoma, by administration of CD40-binding protein, preferably antibody or soluble CD40-ligand

PS Disclosure; Columns 21-24; 21pp; English.

The present sequence represents the amino acid sequence of a novel cytokine ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide, which is expressed by activated CD4<sup>+</sup> T cells. It has an extracellular region at its C-terminus, and an intracellular region at its N-terminus. The protein can be used to produce monoclonal antibodies which in turn bind to CD40-expressing cells. This inhibits binding of soluble CD40 to its ligand CD40L. The monoclonal antibody against CD40L is used to inhibit proliferation of neoplastic cells, and is particularly useful in treating B-cell lymphoma (e.g. where induced after transplants or in other cases of immune deficiency such as AIDS), and also melanoma or carcinoma. Since the monoclonal antibodies inhibit neoplastic cells directly, they may not need to be coupled to a toxin or radioisotope, avoiding toxic effects on normal B cells.

SQ Sequence 261 AA;

Query Match	100.0%;	Score 1335;	DB 18;	Length 261;
Best Local Similarity	100.0%;	Pred. No. 1.3e-128;		

QY	1	METVYQTSPPRSAAATGLPISMKIPMYLLTVFLVLTQMIGSALPAYVYHRRLDKIDEDENH	60
	1	MEETVYQTSPPRSAAATGLPISMKIPMYLLTVFLVLTQMIGSALPAYVYHRRLDKIDEDENH <td>60</td>	60
Db	1	MEETVYQTSPPRSAAATGLPISMKIPMYLLTVFLVLTQMIGSALPAYVYHRRLDKIDEDENH <td>60</td>	60
QY	61	EDFVFEKTTIQRNCNTGERSISLLNCEBIKSQFEGFYKDILNKKEETKENSFEMQKQNP <td>120</td>	120
	61	EDFVFEKTTIQRNCNTGERSISLLNCEBIKSQFEGFYKDILNKKEETKENSFEMQKQNP <td>120</td>	120
Db	61	EDFVFEKTTIQRNCNTGERSISLLNCEBIKSQFEGFYKDILNKKEETKENSFEMQKQNP <td>120</td>	120
QY	121	QIAAHYISASSKRTSYVLQMAEKGYTMSNNLVLTLENGKOLTVYKQGLYTYIAOVTCSN <td>180</td>	180
	121	QIAAHYISASSKRTSYVLQMAEKGYTMSNNLVLTLENGKOLTVYKQGLYTYIAOVTCSN <td>180</td>	180
Db	121	QIAAHYISASSKRTSYVLQMAEKGYTMSNNLVLTLENGKOLTVYKQGLYTYIAOVTCSN <td>180</td>	180
QY	181	REASSQAPFIASILCLKSPGRFERILLRAANTHSSAKPGQOOSIHGQVFELOPQSAFYVN <td>240</td>	240
	181	REASSQAPFIASILCLKSPGRFERILLRAANTHSSAKPGQOOSIHGQVFELOPQSAFYVN <td>240</td>	240
Db	181	REASSQAPFIASILCLKSPGRFERILLRAANTHSSAKPGQOOSIHGQVFELOPQSAFYVN <td>240</td>	240
QY	241	VYDPSQVSHGTGFTSFGLLKL <td>261</td>	261
	241	VYDPSQVSHGTGFTSFGLLKL <td>261</td>	261
Db	241	VYDPSQVSHGTGFTSFGLLKL <td>261</td>	261

## RESULT 6

ID AAW71751 standard; Protein; 261 AA.

AC AAW71751

DT 08-DEC-1998 (first entry)

Human CD40 ligand.

KW Human; CD40 ligand; TNF receptor family; activated T cell;

KW B cell.

OS Homo sapiens.

PN US5817516-A.

PD 06-OCT-1998.

PF 28-APR-1995;

PR 28-APR-1995

PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.

PI Castle B, Kehry M;

DR WPI; 1998-556393/47.

DR N-PSDB; AA61063.

PT	Increased proliferation of B cells in culture - by incubating them
PT	in the presence of membrane-bound CD40 ligand
vv	

Example 1; Fig 1; 37pp; English

The present sequence represents human CD40 ligand which is used in the method of the invention. The method has been developed for proliferating B cells to increase their number at least 100-fold. The method comprises: (a) providing high density, membrane bound CD40 ligand; and (b) culturing one or more B cells in the presence of this ligand. The culture results in a proliferation in the number of B cells of at least 100 fold. Also described is a method as above where the B cells are induced to differentiate into antibody-producing cells in the presence of one or more cytokines. The method can be used for stimulating B-cell proliferation *in vitro* or *in vivo*, e.g. for treating conditions in which B-cell proliferation and activation is suppressed. Eight rounds of division over six days can be achieved, corresponding to a 256-fold increase in cell numbers, which is a vast increase compared to previous culturing methods.

**SQ**      **Sequence**      **261 AA;**

Query Match	100.0%	Score 1335;	DB 18;	Length 261;
Best Local Similarity	100.0%	Pred. No.1.3e-128;		
Matches 261; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MEETNONSPPRAALAGLISIKTIFMYLLTVLLITOMGSLFAAYLHRLDJKEDBERNH	60
Db	1	MEETNONSPPRAALGDLPSIKTIFMYLLTVLLITOMGSLFAAYLHRLDJKEDBERNH	60
QY	61	EDFVPMKTIQRCTNGERSLILNCBEIKSOPEGVKDIMNKERTKXENSFEMQGDONP	120
Db	61	EDFVPMKTIQRCTNGERSLILNCBEIKSOPEGVKDIMNKERTKXENSFEMQGDONP	120
QY	121	QIAAHYISBASKTYSVLQMAEKGYTMSNNLVLTLENGKOLTVRQGLYYITYAQVTFCSN	180
Db	121	QIAAHYISBASKTYSVLQMAEKGYTMSNNLVLTLENGKOLTVRQGLYYITYAQVTFCSN	180
QY	181	REASGCAFFIASLCLKSGFRFERILLRAANTHSSACQCGOOSIHLSGVFELQPGASVFN	240
Db	181	REASGCAFFIASLCLKSGFRFERILLRAANTHSSACQCGOOSIHLSGVFELQPGASVFN	240

Db 181 REASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPGQOSIHGVFELQPGASVFN 240  
QY 241 VTDPQOVSHGTFSTFGLKL 261  
Db 241 VTDPQOVSHGTFSTFGLKL 261

## RESULT 7

AAW41178  
ID AAW41178 standard; Protein; 261 AA.

AC AAW41178;

DT 13-MAY-1998 (first entry)

DE CD40 ligand.

KM leucine zipper; fusion protein production; soluble oligomeric protein;  
KM heterologous mammalian type II transmembrane protein; activated T cell;  
KM heterologous mammalian type I transmembrane protein; antibody production;  
KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen.

OS Homo sapiens.

PN US5716805-A.

PD 10-FEB-1998.

PF 18-MAY-1995; 95US-0446922.

PR 18-MAY-1995; 95US-0446922.

PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

PR 23-OCT-1992; 92US-0969703.

PR 13-AUG-1993; 93US-0107353.

PA (IMMV ) IMMUNEX CORP.

PI Spriggs MK, Srinivasan S;

DR WPI; 1998-144799/13.

DR N-PSDB; AAV12852.

PT Soluble oligomeric fusion proteins - comprising leucine zipper fused

PT to extracellular region of transmembrane protein

PS Example 1; column 21-22; 21pp; English.

XX This sequence represents the the human CD40 ligand (CD40-L).

CC This protein can be used in a fusion protein produced using the

CC method of the invention. The method is for preparing soluble oligomeric

CC protein by culturing a host cell transfected with a vector for the

CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper

CC fused to the N terminus of the extracellular region of a heterologous

CC mammalian type II transmembrane protein or to the C terminus of the

CC extracellular region of a heterologous mammalian type I transmembrane

CC protein. Where the leucine zipper is a peptide comprising at least part

CC of AAW41171 or AAW41172, optionally with conservative amino acid

CC substitutions, provided that the peptide trimerses in solution. A

CC soluble fusion protein comprising the leucine zipper of AAW41171 linked

CC to the extracellular region of CD40-L (a type II transmembrane protein

CC that is found on activated T cells and acts as a ligand for the B-cell

CC antigen CD40) stimulates B-cell proliferation and antibody production in

CC a similar manner to membrane-bound CD40-L. A soluble fusion protein

CC comprising the leucine zipper of AAW41172 linked to the extracellular

CC region of CD27-L (a type II transmembrane protein that binds to the

CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein

CC comprising the extracellular region of CD27 and a human IgG1 Fc region)

CC to EBV-transformed B cells expressing CD27-L.

CC

XX Sequence 261 AA;

SO Query Match 100.0%; Score 1335; DB 19; Length 261;

Best Local Similarity 100.0%; Pred. No. 1,3e-128;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPSAATGPIPSKTIPTVLLITVFLITOMIGSALPAVYLHRLDKIEDERNILH 60

Db 1 MIETYNQTSPPSAATGPIPSKTIPTVLLITVFLITOMIGSALPAVYLHRLDKIEDERNILH 60

QY 61 EDFVFMKTICRNGERSLILNCEERIKSQEPGVKDIIMKEETKENSPEMOKGDNP 120

Db 61 EDFVFMKTICRNGERSLILNCEERIKSQEPGVKDIIMKEETKENSPEMOKGDNP 120

QY 121 QIAAHVISEASSTKTSVLYQMAEKGYTMSNNLVTLENGKOLTVKROGLYTYAQTFCSN 180

Db 121 QIAAHVISEASSTKTSVLYQMAEKGYTMSNNLVTLENGKOLTVKROGLYTYAQTFCSN 180

QY 181 REASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPGQOSIHGVFELQPGASVFN 240

Db 181 REASSQAPFIASLCLKSPGRPERILLRAANTHSSAKPGQOSIHGVFELQPGASVFN 240

QY 241 VTDPQOVSHGTFSTFGLKL 261

Db 241 VTDPQOVSHGTFSTFGLKL 261

## RESULT 8

AA39938  
ID AAY39938 standard; Protein; 261 AA.

AC AAY39938;

DT 13-DEC-1999 (first entry)

DE Human CD40-L protein sequence.

KM CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;

KM binding inhibitor; trimetric CD40-L; anti-Immunoglobulin M;

KM peripheral blood B cell; proliferation inhibitor.

OS Homo sapiens.

PN US5961974-A.

PD 05-OCT-1999.

PF 24-MAY-1994; 94US-0249189.

PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

PR 23-OCT-1992; 92US-0969703.

PA (IMMV ) IMMUNEX CORP.

PI Spriggs MK, Fanslow WC, Armitage RJ;

DR WPI; 1999-579604/49.

DR N-PSDB; AA227525.

PT Anti-human CD40-L ligand monoclonal antibodies -

PT Disclosure; Fig 2; 59pp; English.

XX This sequence represents the human CD40 receptor ligand (CD40-L). The

CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted

CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma

CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40

CC and the ability of trimetric CD40-L and anti-Immunoglobulin M to induce

CC proliferation of peripheral blood B cells.

XX

SO Sequence 261 AA;

Query Match 100.0%; Score 1335; DB 20; Length 261;

Best Local Similarity 100.0%; Pred. No. 1.3e-128;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRLDKIEDERNH 60  
 DB 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRLDKIEDERNH 60  
 QY 61 EDFVFMKTIQRCTNGERSLSLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKDONP 120  
 DB 61 EDFVFMKTIQRCTNGERSLSLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKDONP 120  
 QY 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIAQVTPCSN 180  
 DB 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIAQVTPCSN 180  
 QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHGAVFELQPGASVFN 240  
 DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHGAVFELQPGASVFN 240  
 QY 241 VTDPQOVSHGTGFTSFGLKL 261  
 DB 241 VTDPQOVSHGTGFTSFGLKL 261

## RESULT 9

AA25155

ID AAY25155 standard; protein; 261 AA.

XX AAY25155;

DT 27-AUG-1999 (first entry)

DE Human soluble CD40L protein.

XX CD40L; human; soluble; inhibitor; immune response; T-cell function;  
 KM alloimmunization; immunotherapy; antibody response; model; PBL; Th cell;  
 KM peripheral blood lymphocytes; therapy; B cell; APC; CD40; T-helper cell;  
 KM cytokine secretion; transplantation-induced alloimmune response; anti-HLA;  
 KM systemic lupus erythematosus; SLE; Sjogrens syndrome; Raynaud's syndrome;  
 KM scleroderma myositis; type 1 diabetes; arthritis; rheumatoid arthritis;  
 KM inflammatory bowel disease; uveitis; myasthenia gravis; allergy;  
 KM multiple sclerosis; idiopathic thrombocytopenic purpura; neutrophilic;  
 KM graft vs host disease; dermatological; immunosuppressive; antidiabetic;  
 KM antiinflammatory; antirheumatic; antiarthritic; antiallergic.

XX Homo sapiens.

XX MO9927948-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98MO-CA01105.

XX 28-NOV-1997; 97CA-2223225.

XX (CABL-) CANADIAN BLOOD SERVICES.

XX Crow AR, Freedman J, Lazarus AH;

XX WPI; 1999-404800/34.

XX Use of recombinant human CD40L protein for treating immune diseases

XX Claim 2; Page 41-42; 42pp; English.

XX This invention describes a novel use of a soluble recombinant human CD40L  
 CC (rhCD40L) protein or protein fragment (containing the active binding site  
 CC with CD40) for inhibiting an immune response and T-cell function. The  
 CC invention also describes (1) an immunodeficient mouse model of human  
 CC alloimmunization for testing in vivo effects of an immunotherapy or  
 CC inhibition of a human antibody response, where the mouse model is an  
 CC immunodeficient mouse reconstituted with human peripheral blood  
 CC lymphocytes (PBL) from donors and (2) A method for inhibiting an immune  
 CC response, or T-cell function, in a patient by administering a therapeutic  
 CC amount of rhCD40L or functional fragment. The soluble recombinant CD40L

CC active fragment competes B cell- (or antigen presenting cell (APC)-) CD40  
 CC interaction with CD40L on the Th (T-helper) cells which disallows the Th  
 CC cell to be activated to secrete cytokines (such as Th2 cytokines) which  
 CC thus reduce the transfusion-induced alloimmune response. The rhCD40L or  
 CC its fragment is useful for inhibiting a human anti-HLA alloimmune  
 CC response. Where T-cell function is inhibited the following diseases can  
 CC be treated or prevented: systemic lupus erythematosus (SLE), Sjogrens  
 CC syndrome, scleroderma myositis, Raynaud's syndrome, type 1 diabetes,  
 CC arthritis and rheumatoid arthritis, inflammatory bowel disease, uveitis,  
 CC myasthenia gravis, multiple sclerosis, idiopathic thrombocytopenic  
 CC purpura and graft vs host disease, and allergies dependent on T-cells.  
 CC The development of the model will allow detailed study of the mechanisms  
 CC of alloimmunization and allow the development of new strategies for the  
 CC modulation of human alloimmunization to blood cell antigens.  
 CC Administration of a recombinant 18kDa-CD154 molecule can inhibit an  
 CC alloimmune response. This molecule may have good therapeutic potential  
 CC to inhibit human transfusion-induced alloimmunization. The product of  
 CC the invention has dermatological, immunosuppressive, antiinflammatory,  
 CC antirheumatic, antiarthritic, antidiabetic, neuroprotective and  
 CC antiallergic activity.

SQ Sequence 261 AA;

Query Match 100.0%; Score 1335; DB 20; Length 261;

Best Local Similarity 100.0%; Pred. No. 1,3e-128;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRLDKIEDERNH 60  
 DB 1 MIETYNQTSPPRSAAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRLDKIEDERNH 60  
 QY 61 EDFVFMKTIQRCTNGERSLSLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKDONP 120  
 DB 61 EDFVFMKTIQRCTNGERSLSLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKDONP 120  
 QY 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIAQVTPCSN 180  
 DB 121 QIAAHVISEASSKTSVLOMAEKGYTMSNNLVLTLENGKOLTVKROGLYYIAQVTPCSN 180  
 QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHGAVFELQPGASVFN 240  
 DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHGAVFELQPGASVFN 240  
 QY 241 VTDPQOVSHGTGFTSFGLKL 261  
 DB 241 VTDPQOVSHGTGFTSFGLKL 261

## RESULT 10

AA25155

ID AAY96993 standard; Protein; 261 AA.

XX AAY96993;

XX 31-OCT-2000 (first entry)

XX Human CD40 ligand.

XX CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;  
 KM cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;  
 KM anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic;  
 KM ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;  
 KM dermatological; cytostatic.

XX Homo sapiens.

XX MO200039283-A1.

XX 06-JUL-2000.

XX 22-DEC-1999; 99MO-US30930.

XX 29-DEC-1998; 98US-0114106.



XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 PA Newell MK, Wagner D, Newell E;  
 PI WPI, 2000-452387/39.  
 DR N-PSDB; AAA51745.  
 DR Inducing T cell receptor gene rearrangement for treating autoimmune  
 PT diseases comprises contacting T cells with a CD40-binding agent  
 XX  
 PS Disclosure; Page 47; 50pp; English.  
 XX  
 CC CD40 engagement on T cells can be used to induce T cell receptor  
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40  
 CC engagement can be bought about by contacting CD40 with a CD40-binding  
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used  
 CC in methods for promoting T cell maturation, inhibiting T cell receptor  
 CC rearrangement, inhibiting environmental stress-induced cell death,  
 CC altering the specificity of a T cell towards an antigen, inducing T cell  
 CC reactivity towards an antigen or enhancing environmental stress-induced  
 CC cell death (all claimed). T cell affinity maturation towards a specific  
 CC antigen can be inhibited, especially for a self-antigen in an autoimmune  
 CC disease, which includes rheumatoid arthritis, uveitis, insulin-dependent  
 CC diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease,  
 CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,  
 CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic  
 CC lupus erythematosus. Inducing environmental stress-induced T cell death  
 CC is carried out in a cancerous T cell or a self-reactive T cell where the  
 CC environmental stress is a chemotherapeutic agent (claimed).  
 XX  
 SQ Sequence 261 AA;  
 Query Match 100.0%; Score 1335; DB 21; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETVNTQTSPPRSATGLPISMKIFMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
 DB 1 MIETVNTQTSPPRSATGLPISMKIFMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
 QY 61 EDFVFMKTTIQRCTGERSLSLNCCEIKSQFEGFVNDIMLNKEETKENSFEMQKQDNP 120  
 DB 61 EDFVFMKTTIQRCTGERSLSLNCCEIKSQFEGFVNDIMLNKEETKENSFEMQKQDNP 120  
 QY 121 QIAAHVISEASSKTTSTVLOMAEKGYTMSNNLVTLENGKQLTVKROGLYYIYAQVTFCSN 180  
 DB 121 QIAAHVISEASSKTTSTVLOMAEKGYTMSNNLVTLENGKQLTVKROGLYYIYAQVTFCSN 180  
 QY 181 REASSQAPFIASICLKSPGRFERILRAANTHSSAKPCGQOSIHLGVEFLOPGASVFN 240  
 DB 181 REASSQAPFIASICLKSPGRFERILRAANTHSSAKPCGQOSIHLGVEFLOPGASVFN 240  
 QY 241 VTDPQOVSHGTGFTSFGLLKL 261  
 DB 241 VTDPQOVSHGTGFTSFGLLKL 261

RESULT 11  
 AAB67612 standard; Protein; 261 AA.  
 XX AAB67612;  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Amino acid sequence of human gp39 protein, a CD40 ligand.  
 XX  
 KM gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;  
 KM osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;  
 KM ovariectomy; hysterectomy; lupus nephritis; Takayasu's arteritis;  
 KM Wegener's granulomatosis; nephritis; myositis; scleroderma;  
 KM thrombocytopenia; asthma; lung disease; cancer.

XX Homo sapiens.  
 OS  
 XX  
 PN M0200116180-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000MO-US23276.  
 XX  
 PR 27-AUG-1999; 99US-0151250.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 PA Ahuja SS, Bonewald LF;  
 XX  
 XX  
 DR WPI; 2001-169007/17.  
 DR N-PSDB; AAF5539.  
 XX  
 PT CD40 agonist containing composition, used to reduce bone cell death or  
 PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory  
 PT arthritis -  
 XX  
 PS Claim 3; Page 113-114; 118pp; English.  
 XX  
 CC The present sequence represents a gp39 protein. It is a CD40 ligand.  
 CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,  
 CC and for treating or preventing bone loss in animals, preferably humans,  
 CC at risk of, or undergoing, bone loss. The bone loss is associated with  
 CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal  
 CC estrogen loss, hysterectomy, lupus nephritis, total hysterectomy,  
 CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,  
 CC anti-glomerular basement membrane nephritis, myositis, scleroderma,  
 CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive  
 CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be  
 CC used to treat or prevent bone loss in a subject undergoing, or scheduled  
 CC for, an organ or bone marrow transplant.  
 XX  
 SQ Sequence 261 AA;  
 Query Match 100.0%; Score 1335; DB 22; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETVNTQTSPPRSATGLPISMKIFMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
 DB 1 MIETVNTQTSPPRSATGLPISMKIFMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
 QY 61 EDFVFMKTTIQRCTGERSLSLNCCEIKSQFEGFVNDIMLNKEETKENSFEMQKQDNP 120  
 DB 61 EDFVFMKTTIQRCTGERSLSLNCCEIKSQFEGFVNDIMLNKEETKENSFEMQKQDNP 120  
 QY 121 QIAAHVISEASSKTTSTVLOMAEKGYTMSNNLVTLENGKQLTVKROGLYYIYAQVTFCSN 180  
 DB 121 QIAAHVISEASSKTTSTVLOMAEKGYTMSNNLVTLENGKQLTVKROGLYYIYAQVTFCSN 180  
 QY 181 REASSQAPFIASICLKSPGRFERILRAANTHSSAKPCGQOSIHLGVEFLOPGASVFN 240  
 DB 181 REASSQAPFIASICLKSPGRFERILRAANTHSSAKPCGQOSIHLGVEFLOPGASVFN 240  
 QY 241 VTDPQOVSHGTGFTSFGLLKL 261  
 DB 241 VTDPQOVSHGTGFTSFGLLKL 261

RESULT 12  
 AAB08131 standard; protein; 261 AA.  
 XX AAB08131;  
 XX  
 AC AAB08131;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Human CD40L polypeptide.

XX Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;  
 KM fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
 KM tuberculostatic; cytostatic; human; CD40L.  
 OS Homo sapiens.  
 XX MO200236141-A2.  
 PN 10-MAY-2002.  
 PD 30-OCT-2001; 2001MO-US44834.  
 PF 02-NOV-2000; 2000US-245721P.  
 PR (IMMV ) IMMUNEX CORP.  
 XX  
 PA Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE,  
 PI Thomas EK;  
 DR WPI; 2002-500114/53.  
 XX  
 PT Treating an individual suffering from infection, e.g. inflammation,  
 PT chickenpox or AIDS, by administering a combination of dendritic cell  
 PT mobilization factor or maturation agent, T cell enhancing factor and  
 PT antigen-specific T cells -  
 XX  
 PS Disclosure: Page 39-40; 43pp: English.  
 XX  
 CC The invention relates to treating an individual at risk for or suffering  
 CC from infection with a pathogenic or opportunistic organism. The method  
 CC involves administering a combination of two to five agents comprising:  
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation  
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;  
 CC or (e) activated, antigen-specific T cells. The methods are useful for  
 CC treating an individual at risk for or suffering from infection with a  
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria  
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.  
 CC C. cruzi, which causes Chagas disease). The methods are especially  
 CC useful for treating an individual suffering from immunosuppression by  
 CC enhancing a lymphocyte-mediated immune response. In particular, the  
 CC method is useful for treating inflammations, chickenpox, oral or genital  
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS,  
 CC T cell leukemia or T cell lymphoma. The activated antigen-presenting  
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence  
 CC represents a human CD40L polypeptide fragment, that can be used as a  
 CC dendritic cell maturation agent.  
 CC  
 XX  
 SQ Sequence 261 AA;  
 Query Match 100.0%; Score 1335; DB 23; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRAATGLPISMKIFMYLTIVFLITOMIGSALFAVYLRRLDKIEDERNH 60  
 DB 1 MIETYNQTSPPRAATGLPISMKIFMYLTIVFLITOMIGSALFAVYLRRLDKIEDERNH 60  
 QY 61 BDFVPMKTIQRCTGERSLSLNCERTKQFEGFVDIMANKETKENSFEWQKQDNP 120  
 DB 61 BDFVPMKTIQRCTGERSLSLNCERTKQFEGFVDIMANKETKENSFEWQKQDNP 120  
 QY 121 QIAAHVISEASKTSVLMQAEKGYVTMNNLVTLNGKQLTVKRGGLYYIYAQVTFCSN 180  
 DB 121 QIAAHVISEASKTSVLMQAEKGYVTMNNLVTLNGKQLTVKRGGLYYIYAQVTFCSN 180  
 QY 181 REASSQAPPIASLCLKSPGRFRIILRAANTHSSAPCCQOSIHLGVELPQGSVFN 240  
 DB 181 REASSQAPPIASLCLKSPGRFRIILRAANTHSSAPCCQOSIHLGVELPQGSVFN 240  
 QY 241 VTDPGVSHTGFTSPGLKL 261  
 DB 241 VTDPGVSHTGFTSPGLKL 261

RESULT 13  
 AAM49202  
 ID AAM49202 standard; protein; 261 AA.  
 XX  
 AC AAM49202;  
 XX  
 DT 28-JUN-2002 (first entry)  
 XX  
 DE Human CD145.  
 XX  
 KM Human; CD145; gp39; T-BAM; 5c8 antigen; CD40CR; TRAP;  
 KM monoclonal antibody 5c8; mAb; CD145-antibody complex; 3D structure;  
 KM three dimensional structure; drug design; drug discovery;  
 KM activated T cell; CD40 interaction; T cell dependent immune response;  
 KM agonist; antagonist; immune response; inflammatory response;  
 KM autoimmune disease; allergy; inhibitor response; organ graft rejection;  
 KM B cell cancer; Alzheimer's disease; multiple sclerosis; anti-inflammatory;  
 KM immunosuppressive; antiallergic; cytostatic; dermatological;  
 KM antidiabetic; neuroprotective; antiarteriosclerotic;  
 KM antiviral; antidiabetic; cardiast; antischaeptic; vasodilator;  
 KM antithematic; antithematic; antipsoriatic; immunomodulator;  
 KM receptor; protein co-ordinate data.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 116..261  
 FT /note= "This region is specifically claimed and forms  
 FT part of the crystal of the invention"  
 FT Binding-site 129..132  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 FT Binding-site 142..144  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 FT Binding-site 146  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 FT Binding-site 178  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 FT Binding-site 218  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 FT Modified-site 240  
 FT /note= "N-glycosylated with biantennary complex-type  
 FT carbohydrate"  
 FT Binding-site 245..246  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 FT Binding-site 248..250  
 FT /label= 5c8 epitope  
 FT /note= "Component of the epitope recognised by mAb 5c8  
 FT and humanised mAb 5c8 (AAM49203, AAM49204)"  
 PN MO200218445-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 13-AUG-2001; 2001MO-US27352.  
 XX  
 PR 01-SEP-2000; 2000US-229933P.  
 PR 16-MAR-2001; 2001US-276452P.  
 XX  
 PA (BIOJ ) BIOGEN INC.

XX Karpusas M, Hsu Y, Taylor FR, Zheng Z;  
 XX WPI: 2002-329760/36.  
 XX  
 PT Crystal comprising a CD154 polypeptide complexed with an anti-CD154  
 PT antibody, or its antigen binding fragment, useful for designing drugs  
 PT for the treatment of an autoimmune disease, an allergy, multiple  
 PT sclerosis and Alzheimer's disease -  
 XX  
 PS Claim 4; Fig 8; 470pp; English.

CC The invention relates to a crystal comprising a CD145 polypeptide in  
 CC complex with an anti-CD45 antibody or its antigen-binding fragment, and  
 CC the structure coordinates of such a crystal. In particular, the crystal  
 CC comprises human CD145 (AAM49202) and a humanised version of the murine  
 CC monoclonal antibody 5c8 (husc8; AAM49203, AAM49204). CD145, also known  
 CC as CD40L, gp39, T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type  
 CC II membrane glycoprotein which is transiently expressed on activated T  
 CC cells. It interacts with CD40 which is expressed on mature B cells,  
 CC macrophages, dendritic cells, fibroblasts and activated endothelial  
 CC cells. This CD40:CD145 interaction is required for T cell-dependent  
 CC antibody responses, type I T-helper cell responses, and nitric oxide (NO)  
 CC production by macrophages. NO mediates many of the pro-inflammatory  
 CC activities of macrophages, and disruption of the CD40:CD145 interaction  
 CC via the use of an anti-CD145 antibody has been shown to reduce the  
 CC symptoms of autoimmune and inflammatory conditions. The crystal structure  
 CC of the invention can be used to determine the three dimensional structure  
 CC of the CD145:anti-CD145 antibody complex, and thereby provide information  
 CC about this interaction which may be of use in designing non-antibody  
 CC CD145 agonists and antagonists which modulate the CD40:CD145 interaction.  
 CC Such compounds may be used in the treatment of an unwanted immune  
 CC response, an unwanted inflammatory response, an autoimmune disease, an  
 CC allergy, an inhibitor response to a therapeutic agent, rejection of a  
 CC donor organ, or a B cell cancer. They may be specifically be used to  
 CC treat systemic lupus erythematosus, lupus nephritis, lupus neuritis,  
 CC asthma, chronic obstructive pulmonary disease (COPD), bronchitis,  
 CC emphysema, multiple sclerosis, uveitis, Alzheimer's disease, traumatic  
 CC spinal cord injury, stroke, atherosclerosis, coronary restenosis,  
 CC ischaemic congestive heart failure, cirrhosis, hepatitis C, diabetic  
 CC nephropathy, glomerulonephritis, osteoarthritis, rheumatoid arthritis,  
 CC psoriasis, atopic dermatitis, systemic sclerosis, radiation-induced  
 CC fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma and  
 CC cachexia. The present sequence represents human CD145.  
 CC  
 XX  
 SQ Sequence 261 AA;

Query Match 100.0%; Score 1335; DB 23; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPSAATGPIPSKIFMYLTVFLITOMISALFAVYLHRLKIEBERNLH 60  
 Db 1 MIETYNQTSPPSAATGPIPSKIFMYLTVFLITOMISALFAVYLHRLKIEBERNLH 60  
 QY 61 EDFVFMKTIORCNTGERSLSLNLCEIKSGEGFYKIDMLNKEETKENSEFEMQGDNP 120  
 Db 61 EDFVFMKTIORCNTGERSLSLNLCEIKSGEGFYKIDMLNKEETKENSEFEMQGDNP 120  
 QY 121 QIAAHVISEASSTKTSVYLQMAEKGYTMSNNLVLTLENGKQLTVKRGLYTYAQTFCSN 180  
 Db 121 QIAAHVISEASSTKTSVYLQMAEKGYTMSNNLVLTLENGKQLTVKRGLYTYAQTFCSN 180  
 QY 181 REASSQAPFIASLCLCKSPGRFERILIRAAANTHSSAKPCGQOSIHGCVFEIOPGASVFN 240  
 Db 181 REASSQAPFIASLCLCKSPGRFERILIRAAANTHSSAKPCGQOSIHGCVFEIOPGASVFN 240  
 QY 241 VTDPQVSHGTGFTSPGLKL 261  
 Db 241 VTDPQVSHGTGFTSPGLKL 261

RESULT 14

ABR05350  
 ID ABR05350 standard; protein; 261 AA.  
 XX  
 XX ABR05350;  
 AC  
 DT 05-APR-2002 (first entry)  
 DE Human CD154 amino acid sequence SEQ ID NO:1.  
 XX  
 XX Human; CD154; TNF domain; tumour necrosis factor homologous domain;  
 KW CD40 ligand; immunosuppressive; antiinflammatory; dermatological;  
 KW antiasthmatic; nocitropic; neuroprotective; cerebroprotective;  
 KW antiatherosclerotic; hepatotropic; immunomodulatory; vasotropic;  
 KW antiallergic; ophthalmological; nephrotropic; vitruide; antidiabetic;  
 KW nephrotropic; osteopathic; antiarthritic; antitumor; antineumatic;  
 KW antipsoriatic; CD154 inhibitor; gene therapy; autoimmune disease;  
 KW inflammatory disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key location/Qualifiers  
 FT Domain 116..261  
 FT /label= TNFH  
 FT /note= "tumour necrosis factor homologous domain"  
 XX  
 PN MO200196397-A2.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US18517.  
 XX  
 PR 09-JUN-2000; 2000US-210657P.  
 XX  
 PA (BIOG ) BIOGEN INC.  
 XX  
 PI Hsu Y, Garber E;  
 DR WPI: 2002-139709/18.  
 XX  
 PT Decreasing wildtype CD154 expression on cell surface for treating  
 PT lupus, by introducing nucleotide construct directing expression of  
 PT mutant CD154 lacking portion of tumor necrosis factor homologous domain  
 PT into cell -  
 XX  
 PS Claim 19; Page 5; 41pp; English.

CC The present invention describes a method for decreasing wildtype CD40  
 CC ligand (CD154) expression on a cell surface. The method comprises  
 CC introducing into the cell a nucleic acid construct, (1) that directs  
 CC expression of mutant CD154 lacking at least 5 amino acid residues of  
 CC tumour necrosis factor homologous domain of wildtype CD154, where the  
 CC expressed mutant CD154 binds to wildtype CD154 inside the cell, rendering  
 CC the wild-type CD154 unable to reach cell surface. (1) has antiasthmatic,  
 CC immunosuppressive, antiinflammatory, dermatological, cerebroprotective,  
 CC nocitropic, neuroprotective, antiarthritic, immunomodulator,  
 CC hepatotropic, vasotropic, antiallergic, ophthalmological, nephrotropic,  
 CC vitruide, antidiabetic, nephrotropic, osteopathic, antiarthritic,  
 CC antitumor, antineumatic and antipsoriatic activities. (1) is an  
 CC inhibitor of expression of wildtype CD154 on the surface of a cell, and  
 CC it can be used in gene therapy. The method can be used for treating a  
 CC patient suffering from or predisposed to a CD154-mediated disease, such  
 CC as an autoimmune disease, an inflammatory disease, lupus, systemic lupus  
 CC erythematosus, lupus nephritis, lupus neuritis, asthma, chronic  
 CC obstructive pulmonary disease, bronchitis, emphysema, multiple sclerosis,  
 CC uveitis, Alzheimer's disease, traumatic brain injury, traumatic spinal  
 CC cord injury, stroke, atherosclerosis, coronary restenosis, ischemic  
 CC congestive heart failure, cirrhosis, hepatitis C virus, diabetic  
 CC nephropathy, glomerulonephritis, osteoarthritis, rheumatoid arthritis,  
 CC psoriasis, atopic dermatitis, systemic sclerosis, radiation-induced  
 CC fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma, ocular  
 CC inflammatory disease, graft versus host disease, graft rejection or  
 CC cachexia, by delivering (1) to the patient. The present sequence  
 CC represents wild type human CD154, which is used in the exemplification of

CC the present invention.  
 XX  
 SQ Sequence 261 AA;  
 Query Match 100.0%; Score 1335; DB 23; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSRPSAATGPISMKIFMYLLTVFLITOMIGSALFAYLHRRDLKIEDERNLH 60  
 |||  
 DB 1 MIETYNQTSRPSAATGPISMKIFMYLLTVFLITOMIGSALFAYLHRRDLKIEDERNLH 60

QY 61 EDFVFMKTIQRCNTGERSLSLNCEFIKSGEGFVKDMLNKETKKNSEPMQKQDNP 120  
 |||  
 DB 61 EDFVFMKTIQRCNTGERSLSLNCEFIKSGEGFVKDMLNKETKKNSEPMQKQDNP 120

QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLENGKQLTVRKQGLYYIYAQVTFCSN 180  
 |||  
 DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLENGKQLTVRKQGLYYIYAQVTFCSN 180

QY 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKCGOOSIHLGVFELQPGASVFN 240  
 |||  
 DB 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKCGOOSIHLGVFELQPGASVFN 240

QY 241 VTDPQVSHGTGFTSFGLKL 261  
 |||  
 DB 241 VTDPQVSHGTGFTSFGLKL 261

RESULT 15  
 ABB04674  
 ID ABB04674 standard; protein; 261 AA.  
 XX  
 AC ABB04674;  
 XX  
 DT 06-MAR-2002 (first entry)  
 XX  
 DE Human CD40L extracellular domain amino acid sequence SEQ ID NO:2.  
 XX  
 DE Human; CD40L ligand; extracellular domain; leucine zipper;  
 KW tumour; photodynamic therapy; CD40 binding protein; precancerous cell;  
 KW cytotoxic T lymphocyte response; CTL response; cytostatic; B-lymphoma;  
 KW melanoma; carcinoma; metastatic; cancer; Barrett's oesophagus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200190888-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 25-APR-2001; 2001WO-US13616.  
 XX  
 PR 25-APR-2000; 2000US-199545P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 PI Fanslow WC, Thomas EK;  
 DR WPI, 2002-066404/09.  
 XX  
 PT Treating tumor-bearing or precancerous subject, and inducing memory  
 PT cytotoxic T lymphocyte response specific to tumor in a subject,  
 PT comprises administering CD40 binding protein along with photodynamic  
 PT therapy to subject -  
 XX  
 PS Claim 6; Page 23-24; 24pp; English.  
 XX  
 CC The present invention describes a method for treating a tumour-bearing  
 CC subject or a precancerous subject, and inducing a memory cytotoxic T  
 CC lymphocyte (CTL) response specific to the tumour in a tumour-bearing  
 CC subject. The method involves administering a CD40 binding protein (I) to  
 CC the subject in conjunction with photodynamic therapy (PDT). (I) has  
 CC cytostatic activity. (I), in conjunction with photodynamic therapy

CC (PDT), is useful for treating a tumour-bearing subject or a precancerous  
 CC subject, and inducing a memory CTL response specific to the tumour  
 CC e.g. B-lymphoma, melanoma and carcinoma, in a tumour-bearing subject.  
 CC The method is also useful for treating a wide range of tumours and  
 CC precancerous cells including basal and squamous cells, skin cancer,  
 CC breast cancer, cancers that are metastatic to skin, brain tumours, head  
 CC and neck, stomach, and female genital tract malignancy, cancers and  
 CC precancerous conditions of the oesophagus such as Barrett's oesophagus.  
 CC The present sequence represents human CD40L extracellular domain, which  
 CC can be used in the method of the invention. CD40L is the native ligand  
 CC of CD40 and acts as a CD40 binding protein extracellular domain.

QY 1 MIETYNQTSRPSAATGPISMKIFMYLLTVFLITOMIGSALFAYLHRRDLKIEDERNLH 60  
 |||  
 DB 1 MIETYNQTSRPSAATGPISMKIFMYLLTVFLITOMIGSALFAYLHRRDLKIEDERNLH 60

QY 61 EDFVFMKTIQRCNTGERSLSLNCEFIKSGEGFVKDMLNKETKKNSEPMQKQDNP 120  
 |||  
 DB 61 EDFVFMKTIQRCNTGERSLSLNCEFIKSGEGFVKDMLNKETKKNSEPMQKQDNP 120

QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLENGKQLTVRKQGLYYIYAQVTFCSN 180  
 |||  
 DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLENGKQLTVRKQGLYYIYAQVTFCSN 180

QY 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKCGOOSIHLGVFELQPGASVFN 240  
 |||  
 DB 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKCGOOSIHLGVFELQPGASVFN 240

QY 241 VTDPQVSHGTGFTSFGLKL 261  
 |||  
 DB 241 VTDPQVSHGTGFTSFGLKL 261

RESULT 16  
 ABG22384  
 ID ABG22384 standard; Protein; 263 AA.  
 XX  
 AC ABG22384;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #22375.  
 XX  
 DE Human; chromosome mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 XX  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Drmanac RT, Liu C, Tang YT;  
 DR WPI, 2001-639362/73.  
 XX  
 DR N-PSDB; AAS86571.  
 XX  
 CC New isolated polynucleotide and encoded polypeptides, useful in  
 CC PT diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits and to assess

PT biodiversity

XX Claim 20; SEQ ID NO 52743; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probe,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 263 AA;

Query Match 100.0%; Score 1335; DB 22; Length 263;

Best Local Similarity 100.0%; Pred. No. 1.3e-128; Mismatches 0; Indels 0; Gaps 0;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSAAATGCLPISMKIFMYLTLVPLITOMIGSALPAVYLAHRLDKIEDERNLH 60  
DB 3 MIETYNQTSPPRSAAATGCLPISMKIFMYLTLVPLITOMIGSALPAVYLAHRLDKIEDERNLH 62  
QY 61 EDFVFMKTIORCNTGERSLSLNCBCEIKSQFEGFVADIMLNKEETKENSPEMOKDQNP 120  
DB 63 EDFVFMKTIORCNTGERSLSLNCBCEIKSQFEGFVADIMLNKEETKENSPEMOKDQNP 122  
QY 121 QIAAHVISEASKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGGLYYIYAQVTFCSN 180  
DB 123 QIAAHVISEASKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGGLYYIYAQVTFCSN 182  
QY 181 REASSQAFPIASLCLKSPGRFERILLRAANTHSSAKPCCGQSIIHGGVPELOPGASVFN 240  
DB 183 REASSQAFPIASLCLKSPGRFERILLRAANTHSSAKPCCGQSIIHGGVPELOPGASVFN 242  
QY 241 VTDPQOVSHGTGFTSFGLIKL 261  
DB 243 VTDPQOVSHGTGFTSFGLIKL 263

RESULT 17

AA09122 ID AA09122 standard; Protein; 294 AA.

XX AA09122;

DT 24-SEP-1997 (first entry)

XX CD40 ligand/zipper domain fusion protein mutant 41.

XX CD40 ligand; membrane bound glycoprotein; B cell proliferation;

XX antibody secretion; immunoglobulin B; cytokine; CD40L; mutelin;

XX oligomerisation domain; fusion protein; dimer; trimer.

XX Chimeric - Homo sapiens.

XX Chimeric - Saccharomyces cerevisiae.

XX Synthetic.

XX Key

FT Domain

Location/Qualifiers  
1..33

FT /label= leucine zipper 15M,116T  
FT /note= "Mutant version of yeast GCN4 leucine zipper"  
FT Misc-difference 5  
FT /note= "Wild-type Ile has been replaced by Met"  
FT Misc-difference 16  
FT /note= "Wild-type Ile has been replaced by Thr"  
FT Region 34..294  
FT /label= CD40L

PN MO9640918-A2.

PD 19-DEC-1996.

PF 06-JUN-1996; 96WO-US09632.

PR 07-JUN-1995; 95US-0484624.

PR 07-JUN-1995; 95US-0477733.

PA (IMMV) IMMUNEX CORP.

PI Armltage RJ, Fanslow WC, Gibson MG, Spriggs MK;

PS Srinivasan S;

DR WPI; 1997-052320/05.

PT New CD40 ligand mutein with higher CD40 affinity than native ligand

PT - useful in binding assays, and for therapy of disorders and

PT diseases involving low levels of B cells and antibody secretion

PS Example 4; Page -; 31pp; English.

CC This sequence represents a mutant version of human CD40 ligand/

CC zipper domain fusion protein which is able to bind CD40 in a solid

CC phase binding assay. The random mutations were generated by PCR

CC misincorporation into yeast expression constructs and mutants were

CC selected based on an apparent increase in secretion.

CC (Note: The present sequence does not appear in the specification;

CC it has been produced using the sequences of the leucine zipper and

CC wild-type CD40L which are given on page 23 and pages 20-21.

CC respectively).

XX Sequence 294 AA;

XX Query Match 100.0%; Score 1335; DB 18; Length 294;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-128; Mismatches 0; Indels 0; Gaps 0;

XX Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSAAATGCLPISMKIFMYLTLVPLITOMIGSALPAVYLAHRLDKIEDERNLH 60

DB 34 MIETYNQTSPPRSAAATGCLPISMKIFMYLTLVPLITOMIGSALPAVYLAHRLDKIEDERNLH 93

QY 61 EDFVFMKTIORCNTGERSLSLNCBCEIKSQFEGFVADIMLNKEETKENSPEMOKDQNP 120

DB 94 EDFVFMKTIORCNTGERSLSLNCBCEIKSQFEGFVADIMLNKEETKENSPEMOKDQNP 153

QY 121 QIAAHVISEASKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGGLYYIYAQVTFCSN 180

DB 154 QIAAHVISEASKTSVLOMAEKGYTMSNNLVTLENGKQLTVKRGGLYYIYAQVTFCSN 213

QY 181 REASSQAFPIASLCLKSPGRFERILLRAANTHSSAKPCCGQSIIHGGVPELOPGASVFN 240

DB 214 REASSQAFPIASLCLKSPGRFERILLRAANTHSSAKPCCGQSIIHGGVPELOPGASVFN 273

QY 241 VTDPQOVSHGTGFTSFGLIKL 261

DB 274 VTDPQOVSHGTGFTSFGLIKL 294

Search completed: June 7, 2003, 14:09:41

Job time : 37 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2003, 11:57:28 ; Search time 22.641 seconds  
(without alignments)  
1190.131 Million cell updates/sec

Title: US-09-579-548a-1  
Perfect score: 1335  
Sequence: 1 MIETYNQTSFSAATGLPIS.....TDPQVSHQGTGFTSGLKL 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1335	100.0	261	9	US-10-294-176-2
2	1335	100.0	261	9	US-09-365-940-12
3	1335	100.0	261	9	US-10-218-547-10
4	1335	100.0	261	9	US-10-242-212-2
5	1335	100.0	261	10	US-09-842-745A-2
6	1138.5	85.3	260	9	US-10-218-654-73
7	1112.5	83.3	260	9	US-10-218-654-65
8	1089.5	81.6	273	9	US-09-365-940-21
9	1088	81.5	473	9	US-09-365-940-16
10	1031.5	77.3	260	9	US-09-365-940-2
11	1031.5	77.3	260	10	US-09-842-745A-1
12	921.5	69.0	211	9	US-10-218-654-78
13	889.5	66.6	211	9	US-10-218-654-70
14	808.5	60.6	280	9	US-09-365-940-23
15	766	57.4	149	10	US-09-934-465-16
16	751	56.3	146	9	US-09-343-001-1
17	743	55.7	146	9	US-09-779-050A-10
18	736	55.1	255	9	US-10-185-425-7
19	546	40.9	146	9	US-09-779-050A-11

20	171.5	12.8	316	9	US-10-017-910-4	Sequence 4, Appl1
21	171.5	12.8	316	9	US-10-105-057-2	Sequence 2, Appl1
22	171.5	12.8	316	9	US-10-272-411-19	Sequence 19, Appl1
23	169.5	12.7	294	9	US-09-877-650-11	Sequence 11, Appl1
24	169.5	12.7	294	10	US-09-871-856-11	Sequence 13, Appl1
25	158.5	11.9	317	9	US-09-877-650-11	Sequence 22, Appl1
26	158.5	11.9	317	9	US-10-218-547-22	Sequence 7, Appl1
27	158.5	11.9	317	10	US-09-813-329-7	Sequence 13, Appl1
28	158.5	11.9	317	10	US-09-871-856-13	Sequence 2, Appl1
29	149	11.2	245	9	US-10-017-910-2	Sequence 3, Appl1
30	147.5	11.0	279	12	US-10-066-209-3	Sequence 6, Appl1
31	147.5	11.0	281	8	US-08-916-6258-6	Sequence 8, Appl1
32	147.5	11.0	281	8	US-08-971-3178-8	Sequence 54, Appl1
33	147.5	11.0	281	9	US-10-001-054-54	Sequence 54, Appl1
34	147.5	11.0	281	9	US-10-093-766-54	Sequence 41, Appl1
35	147.5	11.0	281	9	US-10-174-654-11	Sequence 11, Appl1
36	147.5	11.0	281	9	US-10-151-882-41	Sequence 41, Appl1
37	147.5	11.0	281	9	US-10-218-547-20	Sequence 20, Appl1
38	147.5	11.0	281	10	US-09-813-329-17	Sequence 17, Appl1
39	147.5	11.0	281	10	US-09-193-663-8	Sequence 8, Appl1
40	147.5	11.0	281	10	US-09-934-465-1	Sequence 1, Appl1
41	147.5	11.0	281	12	US-10-039-785-66	Sequence 66, Appl1
42	147.5	11.0	281	12	US-10-011-125-4	Sequence 4, Appl1
43	145.5	10.9	291	9	US-10-017-910-6	Sequence 6, Appl1
44	145	10.9	160	9	US-09-779-050A-14	Sequence 14, Appl1
45	130.5	9.8	233	8	US-08-971-317A-5	Sequence 5, Appl1

## ALIGNMENTS

RESULT 1  
US-10-294-176-2  
; Sequence 2, Application US/10294176  
; Publication No. US20030077263A1  
GENERAL INFORMATION:  
APPLICANT: MARASOVSKY, EUGENE  
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Power Macintosh 7200/90  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/294,176  
FILING DATE: 14-NOV-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,448  
FILING DATE: 29-OCT-1999  
APPLICATION NUMBER: 08/763,995  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-10-294-176-2

Query Match 100.0%; Score 1335; DB 9; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2.2e-119;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETVOTSPRSATGPIISMKI FMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
DB 1 MIETVOTSPRSATGPIISMKI FMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
QY 61 EDFVFMKTIOCRNTGERSLSLNCBEEKSQFEGFVKDIMLNKEETKENSFEMQKQDNP 120  
DB 61 EDFVFMKTIOCRNTGERSLSLNCBEEKSQFEGFVKDIMLNKEETKENSFEMQKQDNP 120  
QY 121 QIAAHVISEASSTKTSVLQWAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSTKTSVLQWAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTFCSN 180  
QY 181 REASSQAPFIASICLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVSFELQPGASVFN 240  
DB 181 REASSQAPFIASICLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVSFELQPGASVFN 240  
QY 241 VTDPQVSHGTGFTSFGLKL 261  
DB 241 VTDPQVSHGTGFTSFGLKL 261

## RESULT 2

US-09-365-940-12  
Sequence 12, Application US/09365940  
Publication No. US20030091564A1

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/365,940  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2602-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-365-940-12

Query Match 100.0%; Score 1335; DB 9; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2.2e-119;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETVOTSPRSATGPIISMKI FMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
DB 1 MIETVOTSPRSATGPIISMKI FMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
QY 61 EDFVFMKTIOCRNTGERSLSLNCBEEKSQFEGFVKDIMLNKEETKENSFEMQKQDNP 120  
DB 61 EDFVFMKTIOCRNTGERSLSLNCBEEKSQFEGFVKDIMLNKEETKENSFEMQKQDNP 120  
QY 121 QIAAHVISEASSTKTSVLQWAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSTKTSVLQWAEKGYTMSNNLVLENGKOLTVRQGLYYIYAQVTFCSN 180  
QY 181 REASSQAPFIASICLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVSFELQPGASVFN 240  
DB 181 REASSQAPFIASICLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVSFELQPGASVFN 240  
QY 241 VTDPQVSHGTGFTSFGLKL 261  
DB 241 VTDPQVSHGTGFTSFGLKL 261

## RESULT 3

US-10-218-547-10  
Sequence 10, Application US/10218547  
Publication No. US20030100074A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Re

TITLE OF INVENTION: Human Endokline Alpha

FILE REFERENCE: P561

CURRENT APPLICATION NUMBER: US/10/218,547

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/312,542

PRIOR FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 60/330,761

PRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 57

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10

LENGTH: 261

TYPE: PRT

ORGANISM: human

US-10-218-547-10

Query Match 100.0%; Score 1335; DB 9; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2.2e-119;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETVOTSPRSATGPIISMKI FMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
DB 1 MIETVOTSPRSATGPIISMKI FMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60  
QY 61 EDFVFMKTIOCRNTGERSLSLNCBEEKSQFEGFVKDIMLNKEETKENSFEMQKQDNP 120

Db	61	EDFVFMKTIQR	CNTGERSL	SLNCCBET	KSQ	BEFVVD	IMNKRETI	CKENS	FEFKQKDNP	120	
Qy	121	QIAAHVISEAS	KTTSLV	OWAEKGYTTM	NNLV	YTL	ENGKOL	YTKRQGL	YTYTAQVTPCSN	180	
Db	121	QIAAHVISEAS	KTTSLV	OWAEKGYTTM	NNLV	YTL	ENGKOL	YTKRQGL	YTYTAQVTPCSN	180	
Qy	181	REASSQAEPI	IASLCL	CKSPGR	FERIL	IL	RAANTHSS	APCCQSS	IHLGVEFELQ	PGASVFN	240
Db	181	REASSQAEPI	IASLCL	CKSPGR	FERIL	IL	RAANTHSS	APCCQSS	IHLGVEFELQ	PGASVFN	240
Qy	241	VTDPSSQVSH	GTGFTS	PGILKL						261	
Db	241	VTDPSSQVSH	GTGFTS	PGILKL						261	

```

RESULT 4
US-10-242-212-2
; Sequence 2, Application US/10242212
; Publication No. US2003009644A1
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEENA
; APPLICANT: BONEWALD, LYNDIA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/10/242,212
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US/09/645,926
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 261
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-242-212-2

```

Query Match	100.0%;	Score 1335;	DB 9;	Length 261;
Best Local Similarity	100.0%;	Pred. No. 2.2e-119;		
Matches 261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MIETNONSPPRAAAGLPISMKIFMWLLTVFLITOMIGSALFPAVYLHRRIDKIEDERNLH	60
Db	1	MIETNONSPPRAAAGLPISMKIFMWLLTVFLITOMIGSALFPAVYLHRRIDKIEDERNLH	60
QY	61	EDFVEMKTIQR CNTGERSL SLNCEBIKSGFEGFVADIMLNKETKKENS FEMQKQDNP	120
Db	61	EDFVEMKTIQR CNTGERSL SLNCEBIKSGFEGFVADIMLNKETKKENS FEMQKQDNP	120
QY	121	QIAAHVISEASKTSV LQMAEKGYTMSNNLVTLENGQQLTVKROGLYYTAAQVTFCSN	180
Db	121	QIAAHVISEASKTSV LQMAEKGYTMSNNLVTLENGQQLTVKROGLYYTAAQVTFCSN	180
QY	181	REASSQAEPFIASLCLCKSPGRFERILLRANTHSSAKPCCQOSIHLGQVPELOGASVFPN	240
Db	181	REASSQAEPFIASLCLCKSPGRFERILLRANTHSSAKPCCQOSIHLGQVPELOGASVFPN	240
QY	241	VTDPBSQVSHGTCGTSFGLLKL	261
Db	241	VTDPBSQVSHGTCGTSFGLLKL	261

RESULT 5  
US-09-842-745A-2  
; Sequence 2, Application US/09842745A  
; Patent No. US20020041864A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanslow III, William C.  
; APPLICANT: Thomas, Elaine K.  
; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING PHOTODYNAMIC  
; TITLE OF INVENTION: THERAPY  
; FILE REFERENCE: 2922-A

```

1  CURRENT APPLICATION NUMBER: US/09/842,745A-1
2  CURRENT FILING DATE: 2001-08-01
3  NUMBER OF SEQ ID NOS: 3
4  SOFTWARE: PatentIn Ver. 2.0
5  SEQ ID NO: 2
6  LENGTH: 261
7  TYPE: PRT
8  ORGANISM: Homo sapiens
9  US-09-842-745A-2

```

Query Match	100.0%;	Score 1335;	DB 10;	Length 261;
Best Local Similarity	100.0%;	Prod No 3	2010	

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MIETYNQSPSPSAATAGLISMKIIPAYLLTVFLITOMISGALPAVYLHRLDLDKIEDERNH	60
Db	1	MIETYNQSPSPSAATAGLIPISMKIPAYLLTVFLITOMISGALPAVYLHRLDLDKIEDERNH	60
QY	61	EDFVPMKTIQPCNTGERSLSLNCBEEKSQEPGVKIDMLNTEETKENSFEMQKDQNP	120
Db	61	EDFVPMKTIQPCNTGERSLSLNCBEEKSQEPGVKIDMLNTEETKENSFEMQKDQNP	120
QY	121	QIAAHVISEASKTTSVLOMAEKGYTMSNNLYTLENGKOLTVKQGLYYTAAQVTFCSN	180
Db	121	QIAAHVISEASKTTSVLOMAEKGYTMSNNLYTLENGKOLTVKQGLYYTAAQVTFCSN	180
QY	181	REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCQOOSIHLGGVETLQPGASVFVN	240
Db	181	REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCQOOSIHLGGVETLQPGASVFVN	240
QY	241	VTPDSQVSHGTGFTSPGLKL	261
Db	241	VTPDSQVSHGTGFTSPGLKL	261

RESULT 6  
US-10-218-654-73

```

? Sequence 73, Application US/10218654
? Publication No. US20030095609A1
? GENERAL INFORMATION:
? APPLICANT: Sim, Gek-Kee
? APPLICANT: Yang, Shumin
? APPLICANT: Drelitz, Matthew J.
? APPLICANT: Wonderling, Ramani S.
? TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
? TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
? FILE REFERENCE: IM-2-C1
? CURRENT APPLICATION NUMBER: US/10/218,654
? CURRENT FILING DATE: 2002-08-13
? PRIOR APPLICATION NUMBER: US/09/322,409
? PRIOR FILING DATE: 1999-05-28
? PRIOR APPLICATION NUMBER: 60/087,306
? PRIOR FILING DATE: 1998-05-29
? NUMBER OF SEQ ID NOS: 154
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 73
? LENGTH: 260
? TYPE: PRT
? ORGANISM: Felis catus
? /S-10-218-654-73

```

Query Match	85.3%;	Score 1138.5;	DB 9;	Length 260;
Best Local Similarity	85.1%;	Pred. No. 1.2e-100;		
Matches 22;	Conservative 18;	Mismatches 20;	Indels 1;	Gaps 1;

[illegible]



```
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLKNGKQLTVKROGLYYIYAQVTFCSN 180
DB 120 RIAAHVISEASSSTASVLPQAPKGYTTISSNLVTLKNGKQLAVKROGLYYIYAQVTFCSN 179
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVPFELQPGASVFN 240
DB 180 REASSQAPFIASLCLKSPSSSERVLLRAANARSSKPCGOOSIHLGVPFELHFGASVFN 239
QY 241 VTDPQOVSHGTGFTSFGLLKL 261
DB 240 VTDPQOVSHGTGFTSFGLLKL 260

RESULT 7
US-10-218-654-65
; Sequence 65, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreltz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 260
; TYPE: PRT
; ORGANSIM: Canis familiaris
US-10-218-654-65

Query Match 83.3%; Score 1112.5; DB 9; Length 260;
Best Local Similarity 82.8%; Pred. No. 3.7e-98;
Matches 216; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 1 METVNOTSPRSAAATGLPIISMKTIFMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLH 60
DB 1 METVYQTAPRSVATGPVPMKIFMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLY 60
QY 61 EDFVFMKTIOKCKRGESLSLNCBEIKSQFEGFVDIMLNKEPKKNSPFEMOKGQDP 120
DB 61 EDFVFMKTIOKCKRGESLSLNCBEIKSQFEAFLEIMLN-NEMKKEENIAMQKQDP 119
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLKNGKQLTVKROGLYYIYAQVTFCSN 180
DB 120 RIAAHVISEASSSTASVLPQAPKGYTTISSNLVTLKNGKQLAVKROGLYYIYAQVTFCSN 179
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVPFELQPGASVFN 240
DB 180 REASSQAPFIASLCLKSPSSSERVLLRAANARSSKPCGOOSIHLGVPFELHFGASVFN 239
QY 241 VTDPQOVSHGTGFTSFGLLKL 261
DB 240 VTDPQOVSHGTGFTSFGLLKL 260

RESULT 8
US-09-365-940-21
; Sequence 21, Application US/09365940
; Publication No. US20030091564A1
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: PANSLOW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
```

```
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/365,940
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-365-940-21

Query Match 81.6%; Score 1089.5; DB 9; Length 273;
Best Local Similarity 89.3%; Pred. No. 6.2e-96;
Matches 217; Conservative 5; Mismatches 14; Indels 7; Gaps 1;

QY 19 ISMKITMYLLTVFLITOMIGSALFVYLRRLDKIEDERNLHEDFVFMKTIOKNTGERS 78
DB 38 ILSKIYHENEIARIKTLIGERTS-----DKIEDERNLHEDFVFMKTIOKNTGERS 90
QY 79 ILSLNCBEIKSQFEGFVDIMLNKEPKKNSPFEMOKGQDPQIAAHVISEASSKTTSVL 138
DB 91 ILSLNCBEIKSQFEGFVDIMLNKEPKKNSPFEMOKGQDPQIAAHVISEASSKTTSVL 150
QY 139 QMAEKGYTMSNNLVTLKNGKQLTVKROGLYYIYAQVTFCSNREASSQAPFIASLCLKSP 198
DB 151 QMAEKGYTMSNNLVTLKNGKQLTVKROGLYYIYAQVTFCSNREASSQAPFIASLCLKSP 210
QY 199 GRFERILLRAANTHSSAKPCGOOSIHLGVPFELQPGASVFNVTDPQOVSHGTGFTSFGL 258
DB 211 GRFERILLRAANTHSSAKPCGOOSIHLGVPFELQPGASVFNVTDPQOVSHGTGFTSFGL 270
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Db 271 LKL 273

## RESULT 9

US-09-365-940-16  
; Sequence 16, Application US/09365940  
; Publication No. US20030091564A1  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLON, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/365,940  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEO ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-365-940-16

Query Match 81.5%; Score 1088, DB 9, Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.9e-95;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 DKIEDENHEDFEMKTCRCNGERSLSLNGCEIKSQEFGVKDMLMKETKRENS 110  
DB 263 DKIEDENHEDFEMKTCRCNGERSLSLNGCEIKSQEFGVKDMLMKETKRENS 322

QY 111 FEMQKGDONFOIAAHVISEBASSTKTSYLTQWAEKGYTMSNNLVTLENGKQULTVRQGLY 170  
DB 323 FEMQKGDONFOIAAHVISEBASSTKTSYLTQWAEKGYTMSNNLVTLENGKQULTVRQGLY 382  
QY 171 IYAQVTFCSNREASQAPFIASLCSPGPERILLPAANTHSSAKCGOOSIHLGVFE 230  
DB 383 IYAQVTFCSNREASQAPFIASLCSPGPERILLPAANTHSSAKCGOOSIHLGVFE 442  
QY 231 LOPGASVFVNTDPSOVSHGTGFTSPGLKL 261  
DB 443 LOPGASVFVNTDPSOVSHGTGFTSPGLKL 473

## RESULT 10

US-09-365-940-2  
; Sequence 2, Application US/09365940  
; Publication No. US20030091564A1  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLON, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/365,940  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEO ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 260 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-365-940-2

Query Match 77.3%; Score 1031.5; DB 9; Length 260;  
Best Local Similarity 77.4%; Pred. No. 2e-90;  
Matches 202; Conservative 23; Mismatches 35; Indels 1; Gaps 1;  
QY 1 MIETNOTSPRSATGPIISMKI FMYLLTVLTOMIGSALPAYILHRLDKIEDERLH 60  
DB 1 MIETSPSPRSVATGIPASMKI FMYLLTVLTOMIGSVLPAYILHRLDKVEEVLH 60  
QY 61 EDFVFMKTIO RCNTGERSLSLNCCEIKSQFEGVKDMLNKEETKENS FEMOKGONP 120  
DB 61 EDFVFIKKLCKCKNGEGSLINLNCCEMRQPEDLVKDTITLNKEE-KENS FEMQGDDEP 119  
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTENGKQLTVRKQGLYTYIAQVTFCSN 180  
DB 120 QIAAHVISEANSNAASVLOMAKGYTMTKSNLVMLENGKQLTVRKGLYVYVYQVTFCSN 179  
QY 181 REASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHLGGVFELOPGASVFN 240  
DB 180 REPSQRPFIIVGLMLKPSGSRILLKRAHTSSSOLCEQOSVHLGGVFELOPGASVFN 239  
QY 241 VTDPQVSHGTGFTSFGLKL 261  
DB 240 VTEASQVIRHVGFSSFGLLKL 260

RESULT 11  
US-09-842-745A-1  
; Sequence 1, Application US/09842745A  
; Patent No. US20020041864A1  
; GENERAL INFORMATION:  
; APPLICANT: Farnslow III, William C.  
; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING PHOTODYNAMIC  
; FILE REFERENCE: 2922-A  
; CURRENT APPLICATION NUMBER: US/09/842, 745A  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-842-745A-1

Query Match 77.3%; Score 1031.5; DB 10; Length 260;  
Best Local Similarity 77.4%; Pred. No. 2e-90;  
Matches 202; Conservative 23; Mismatches 35; Indels 1; Gaps 1;  
QY 1 MIETNOTSPRSATGPIISMKI FMYLLTVLTOMIGSALPAYILHRLDKIEDERLH 60  
DB 1 MIETSPSPRSVATGIPASMKI FMYLLTVLTOMIGSVLPAYILHRLDKVEEVLH 60  
QY 61 EDFVFMKTIO RCNTGERSLSLNCCEIKSQFEGVKDMLNKEETKENS FEMOKGONP 120  
DB 61 EDFVFIKKLCKCKNGEGSLINLNCCEMRQPEDLVKDTITLNKEE-KENS FEMQGDDEP 119  
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTENGKQLTVRKQGLYTYIAQVTFCSN 180  
DB 120 QIAAHVISEANSNAASVLOMAKGYTMTKSNLVMLENGKQLTVRKGLYVYVYQVTFCSN 179  
QY 181 REASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHLGGVFELOPGASVFN 240  
DB 180 REPSQRPFIIVGLMLKPSGSRILLKRAHTSSSOLCEQOSVHLGGVFELOPGASVFN 239  
QY 241 VTDPQVSHGTGFTSFGLKL 261  
DB 240 VTEASQVIRHVGFSSFGLLKL 260

RESULT 12  
US-10-218-654-78

Sequence 78, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shunlin  
; APPLICANT: Dretz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-218-654-78

Query Match 69.0%; Score 921.5; DB 9; Length 211;  
Best Local Similarity 84.4%; Pred. No. 4.6e-80;  
Matches 179; Conservative 15; Mismatches 17; Indels 1; Gaps 1;  
QY 50 LDKIEDERNLHEDVFMKTIO RCNTGERSLSLNCCEIKSQFEGVKDMLNKEETKEN 109  
DB 1 LDKIEDERNLYEDVFMKTIO RCNTGERSLSLNCCEIKSQFEGVKDMLNKEETKEN 59  
QY 110 SFEMOKGONPQIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTENGKQLTVRKQGLY 169  
DB 60 NVAMOKGDDOPRAAHVISEASSSTASVLOMAKGYTITSSNLVLTENGKQLAVERKGLY 119  
QY 170 YTYAQTFFCSNREASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHLGGV 229  
DB 120 YTYAQTFFCSNREASSQAPFIASLCLKSPGSRVILLRANHTSSAKPCGOOSIHLGGV 179  
QY 230 ELPGASVFNVTDPQVSHGTGFTSFGLKL 261  
DB 180 ELHPGASVFNVTDPQVSHGTGFTSFGLKL 211

RESULT 13  
US-10-218-654-70  
; Sequence 70, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shunlin  
; APPLICANT: Dretz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-218-654-70

Query Match 66.6%; Score 889.5; DB 9; Length 211;  
Best Local Similarity 81.1%; Pred. No. 5.2e-77;



Sat Jun 7 13:51:25 2003

us-09-579-548a-1.ra1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2003, 14:11:16 ; Search time 26 Seconds

(without alignments)  
295,361 Million cell updates/sec

Title: US-09-579-548A-1

Perfect score: 1335

Sequence: 1 MIETRYNOTSPRSATGIPIS.....TDPQVSHGTGTFSGFLKL 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/prodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCITUS.COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1335	100.0	261	1	US-07-940-605A-2
2	1335	100.0	261	1	US-08-184-422-8
3	1335	100.0	261	1	US-08-360-923A-2
4	1335	100.0	261	1	US-08-446-922-4
5	1335	100.0	261	2	US-08-431-055-4
6	1335	100.0	261	2	US-08-690-096-2
7	1335	100.0	261	2	US-08-249-189-12
8	1335	100.0	261	2	US-08-484-624A-12
9	1335	100.0	261	2	US-08-477-733B-12
10	1335	100.0	261	3	US-08-763-995-2
11	1335	100.0	261	3	US-09-088-913A-12
12	1335	100.0	261	3	US-08-769-819-12
13	1335	100.0	261	4	US-08-770-974-12
14	1335	100.0	261	4	US-08-858-197-4
15	1335	100.0	261	4	US-08-770-981-12
16	1335	100.0	261	4	US-09-399-106-12
17	1335	100.0	261	5	PCT-US93-10034-4
18	1335	100.0	261	5	US-08-446-922-11
19	1089.5	81.6	273	2	US-08-249-189-21
20	1089.5	81.6	273	2	US-08-484-624A-21
21	1089.5	81.6	273	2	US-08-477-733B-21
22	1089.5	81.6	273	3	US-09-088-913A-21
23	1089.5	81.6	273	4	US-08-769-819-21
24	1089.5	81.6	273	4	US-08-770-974-21
25	1089.5	81.6	273	4	US-08-770-981-21
26	1089.5	81.6	273	4	US-09-399-106-21
27	1089.5	81.6	273	4	US-09-399-106-21

28	1088	81.5	473	2	US-08-249-189-16	Sequenc
29	1088	81.5	473	2	US-08-484-624A-16	Sequenc
30	1088	81.5	473	3	US-08-477-733B-16	Sequenc
31	1088	81.5	473	3	US-09-088-913A-16	Sequenc
32	1088	81.5	473	4	US-08-769-819-16	Sequenc
33	1088	81.5	473	4	US-08-770-974-16	Sequenc
34	1088	81.5	473	4	US-08-770-981-16	Sequenc
35	1088	81.5	473	4	US-09-399-106-16	Sequenc
36	1031.5	77.3	260	1	US-08-446-922-6	Sequenc
37	1031.5	77.3	260	2	US-08-249-189-2	Sequenc
38	1031.5	77.3	260	2	US-08-484-624A-2	Sequenc
39	1031.5	77.3	260	2	US-08-477-733B-2	Sequenc
40	1031.5	77.3	260	3	US-09-088-913A-2	Sequenc
41	1031.5	77.3	260	4	US-08-769-819-2	Sequenc
42	1031.5	77.3	260	4	US-08-770-974-2	Sequenc
43	1031.5	77.3	260	4	US-08-770-981-2	Sequenc
44	1031.5	77.3	260	4	US-09-399-106-2	Sequenc
45	1031.5	77.3	260	5	PCT-US93-10034-6	Sequenc

#### ALIGNMENTS

RESULT 1  
US-07-940-605A-2

Sequence 2, Application US/07940605A

Patent No. 5540926

GENERAL INFORMATION:

APPLICANT: ARUFFO, ALJANDRO

APPLICANT: HOLENBAUGH, DIANE

APPLICANT: LEDBETTER, JEFFREY A.

TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/940,605A

FILING DATE: 04-SEP-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-940-605A-2

Query Match

Best Local Similarity 100.0%; Score 1335; DB 1; Length 261;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 1 MIETRYNOTSPRSATGIPISKIMFYLLTVLITOMIGSALFAVYLRRLDIEDERNH 60

DB 1 MIETRYNOTSPRSATGIPISKIMFYLLTVLITOMIGSALFAVYLRRLDIEDERNH 60

QY 61 EDFVFMKTICRNTGERSLSLNCCEIISQFEGFVKDIMNKETTKENSFEMOKGQNP 120  
DB 61 EDFVFMKTICRNTGERSLSLNCCEIISQFEGFVKDIMNKETTKENSFEMOKGQNP 120  
QY 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVTLNGKOLTVRQGLYYTYAQTFCSN 180  
DB 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVTLNGKOLTVRQGLYYTYAQTFCSN 180  
QY 181 REASSQAPFTASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVFELQPGASVFN 240  
DB 181 REASSQAPFTASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVFELQPGASVFN 240  
QY 241 VTDPSQVSHGTGFTSFGLKL 261  
DB 241 VTDPSQVSHGTGFTSFGLKL 261

## RESULT 2

US-08-184-422-8  
Sequence 8, Application US/08184422  
Patent No. 5565321  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVISON, BARRY  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSLOW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
TITLE OF INVENTION: IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS Word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/184,422  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-184-422-8

Query Match 100.0%; Score 1335; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MIETVNTSPRSATGPIPIKMKIFMYLLTVFLITQWIGSALFAVYLRRLDKIEDERNLH 60  
DB 1 MIETVNTSPRSATGPIPIKMKIFMYLLTVFLITQWIGSALFAVYLRRLDKIEDERNLH 60

QY 61 EDFVFMKTICRNTGERSLSLNCCEIISQFEGFVKDIMNKETTKENSFEMOKGQNP 120  
DB 61 EDFVFMKTICRNTGERSLSLNCCEIISQFEGFVKDIMNKETTKENSFEMOKGQNP 120  
QY 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVTLNGKOLTVRQGLYYTYAQTFCSN 180  
DB 121 QIAAHVISEASSKTTSTVLQWAEKGYTMSNNLVTLNGKOLTVRQGLYYTYAQTFCSN 180  
QY 181 REASSQAPFTASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVFELQPGASVFN 240  
DB 181 REASSQAPFTASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLGVFELQPGASVFN 240  
QY 241 VTDPSQVSHGTGFTSFGLKL 261  
DB 241 VTDPSQVSHGTGFTSFGLKL 261

## RESULT 3

US-08-360-923A-2  
Sequence 2, Application US/08360923A  
Patent No. 5674492  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MORPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,923A  
FILING DATE: December 21, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2818-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-360-923A-2

Query Match 100.0%; Score 1335; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MIETVNTSPRSATGPIPIKMKIFMYLLTVFLITQWIGSALFAVYLRRLDKIEDERNLH 60  
DB 1 MIETVNTSPRSATGPIPIKMKIFMYLLTVFLITQWIGSALFAVYLRRLDKIEDERNLH 60

QY 61 EDFVFMKTIOKNTGERSLSLNCBEIKSQFEGFYKD IMLNKEETKENS FEMQKGDNP 120  
DB 61 EDFVFMKTIOKNTGERSLSLNCBEIKSQFEGFYKD IMLNKEETKENS FEMQKGDNP 120  
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVRKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVRKQGLYYIYAQVTFCSN 180  
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGGVFELQPGASVFN 240  
DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGGVFELQPGASVFN 240  
QY 241 VTDPSQVSHGTGTFSTGLKL 261  
DB 241 VTDPSQVSHGTGTFSTGLKL 261

## RESULT 4

US-08-446-922-4  
Sequence 4, Application US/08446922  
Patent No. 5716805  
GENERAL INFORMATION:  
APPLICANT: Springs, Melanie  
APPLICANT: Srinivasan, Subhashini  
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,922  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/107,353  
FILING DATE: 08-13-93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-922-4

Query Match 100.0%; Score 1335; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEYNTQNSPRSAATGALPISMKIFMYLLTVFLITQMIGSALPAVYLHRLDKIEDERNH 60  
DB 1 MIEYNTQNSPRSAATGALPISMKIFMYLLTVFLITQMIGSALPAVYLHRLDKIEDERNH 60  
QY 61 EDFVFMKTIOKNTGERSLSLNCBEIKSQFEGFYKD IMLNKEETKENS FEMQKGDNP 120  
DB 61 EDFVFMKTIOKNTGERSLSLNCBEIKSQFEGFYKD IMLNKEETKENS FEMQKGDNP 120

QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVRKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVRKQGLYYIYAQVTFCSN 180  
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGGVFELQPGASVFN 240  
DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGGVFELQPGASVFN 240  
QY 241 VTDPSQVSHGTGTFSTGLKL 261  
DB 241 VTDPSQVSHGTGTFSTGLKL 261

## RESULT 5

US-08-431-055-4  
Sequence 4, Application US/08431055  
Patent No. 5817516  
GENERAL INFORMATION:  
APPLICANT: KERRY, MERILYN R  
APPLICANT: CASTLE, BRIAN E  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,055  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,580  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-431-055-4

Query Match 100.0%; Score 1335; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEYNTQNSPRSAATGALPISMKIFMYLLTVFLITQMIGSALPAVYLHRLDKIEDERNH 60  
DB 1 MIEYNTQNSPRSAATGALPISMKIFMYLLTVFLITQMIGSALPAVYLHRLDKIEDERNH 60  
QY 61 EDFVFMKTIOKNTGERSLSLNCBEIKSQFEGFYKD IMLNKEETKENS FEMQKGDNP 120  
DB 61 EDFVFMKTIOKNTGERSLSLNCBEIKSQFEGFYKD IMLNKEETKENS FEMQKGDNP 120  
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVRKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVRKQGLYYIYAQVTFCSN 180

QY 181 REASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHGCVFELQPGASVFN 240  
Db 181 REASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHGCVFELQPGASVFN 240  
QY 241 VTDPQVSHGTGFTSFGLKL 261  
Db 241 VTDPQVSHGTGFTSFGLKL 261

## RESULT 6

US-08-690-096-2  
; Sequence 2, Application US/08690096  
; Patent No. 5945513  
; GENERAL INFORMATION:  
; APPLICANT: ARUFFO, ALEJANDRO  
; APPLICANT: HOLLEBAUGH, DIANE  
; APPLICANT: LEDBETTER, JEFFREY A.  
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penmie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/690,096  
; FILING DATE: 31-JUL-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/940,605  
; FILING DATE: 04-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8664/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-690-096-2

Query Match 100.0%; Score 1335; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSATGPIPSMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERNLH 60  
Db 1 MIETYNQTSPPRSATGPIPSMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERNLH 60  
QY 61 EDFPMFTIORCNTGERSLSLNCEETKSQFEGVYKIMLNKETKXNSFEMQKQDNP 120  
Db 61 EDFPMFTIORCNTGERSLSLNCEETKSQFEGVYKIMLNKETKXNSFEMQKQDNP 120  
QY 121 QIAAHVISEASSTKTSVLOMAEKGYTMSNNLVTLLENGKOLTVRKQGLYYTAAVTECSN 180  
Db 121 QIAAHVISEASSTKTSVLOMAEKGYTMSNNLVTLLENGKOLTVRKQGLYYTAAVTECSN 180  
QY 181 REASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHGCVFELQPGASVFN 240  
Db 181 REASSQAPFIASLCLKSPGRFERILLRANHTSSAKPCGOOSIHGCVFELQPGASVFN 240

QY 241 VTDPQVSHGTGFTSFGLKL 261  
Db 241 VTDPQVSHGTGFTSFGLKL 261

## RESULT 7

US-08-249-189-12  
; Sequence 12, Application US/08249189  
; Patent No. 5961974  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSTLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,189  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-249-189-12

Query Match 100.0%; Score 1335; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSATGPIPSMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERNLH 60  
Db 1 MIETYNQTSPPRSATGPIPSMKIFMYLLTVFLITOMIGSALFAVYLRRLDKIEDERNLH 60  
QY 61 EDFPMFTIORCNTGERSLSLNCEETKSQFEGVYKIMLNKETKXNSFEMQKQDNP 120  
Db 61 EDFPMFTIORCNTGERSLSLNCEETKSQFEGVYKIMLNKETKXNSFEMQKQDNP 120



Qy 121 QIAHVISSEASKTTSVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
Db 121 QIAHVISSEASKTTSVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
Qy 181 REASSQAPFLASLCLKSPGRFRERILLRANHTSSAKPCGQOSIHLGVFELQPGASVFN 240  
Db 181 REASSQAPFLASLCLKSPGRFRERILLRANHTSSAKPCGQOSIHLGVFELQPGASVFN 240  
Qy 241 VTDPQVSHGTGFTSPGLKL 261  
Db 241 VTDPQVSHGTGFTSPGLKL 261

## RESULT 8

US-08-484-624A-12  
; Sequence 12, Application US/08484624A  
; Patent No. 5962406  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,624A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: June 07, 1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-484-624A-12

Query Match 100.0%; Score 1335; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIETYNQTSPPSAATGPEISMKIFMYLLTVFLITOMIGSALFAYLHRLDKIEDERMLH 60  
Db 1 MIETYNQTSPPSAATGPEISMKIFMYLLTVFLITOMIGSALFAYLHRLDKIEDERMLH 60  
Qy 61 EDFVFMKTICQNTGERSLSLNCERIKSQPEGVKQIMLKEETKKNSEFEMQKQDNP 120  
Db 61 EDFVFMKTICQNTGERSLSLNCERIKSQPEGVKQIMLKEETKKNSEFEMQKQDNP 120  
Qy 121 QIAHVISSEASKTTSVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
Db 121 QIAHVISSEASKTTSVLQMAEKGYTMSNNLVTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
Qy 181 REASSQAPFLASLCLKSPGRFRERILLRANHTSSAKPCGQOSIHLGVFELQPGASVFN 240  
Db 181 REASSQAPFLASLCLKSPGRFRERILLRANHTSSAKPCGQOSIHLGVFELQPGASVFN 240  
Qy 241 VTDPQVSHGTGFTSPGLKL 261  
Db 241 VTDPQVSHGTGFTSPGLKL 261

## RESULT 9

US-08-477-733B-12  
; Sequence 12, Application US/08477733B  
; Patent No. 5981724  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,733B  
; FILING DATE: June 07, 1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,189  
; FILING DATE: May 24, 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-733B-12

Query Match 100.0%; Score 1335; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRAAGLPISMKIFMYLLTVFLITQMGALPAVYIHRRLDKIEDERNIH 60  
DB 1 MIETYNQTSPPRAAGLPISMKIFMYLLTVFLITQMGALPAVYIHRRLDKIEDERNIH 60  
QY 61 EDFVFMKTIORCNTGRSISLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKGDNP 120  
DB 61 EDFVFMKTIORCNTGRSISLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKGDNP 120  
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKQLTVKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKQLTVKQGLYYIYAQVTFCSN 180  
QY 181 REASSOAPFIASLCLKSGRFRERILLRAANTHSSAKPGQOOSIHJGVFELPGASVFN 240  
DB 181 REASSOAPFIASLCLKSGRFRERILLRAANTHSSAKPGQOOSIHJGVFELPGASVFN 240  
QY 241 VTDPQOVSHGTGFTSFGLKL 261  
DB 241 VTDPQOVSHGTGFTSFGLKL 261

RESULT 10  
US-08-763-995-2  
Sequence 2, Application US/08763995  
Patent No. 6017527  
GENERAL INFORMATION:  
APPLICANT: MARASKOVSKY, EUGENE  
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Macintosh 7200/90  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763,995  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US98 08/677,762  
FILING DATE: 10 JUL 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-763-995-2

Query Match 100.0%; Score 1335; DB 3; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRAAGLPISMKIFMYLLTVFLITQMGALPAVYIHRRLDKIEDERNIH 60  
DB 1 MIETYNQTSPPRAAGLPISMKIFMYLLTVFLITQMGALPAVYIHRRLDKIEDERNIH 60  
QY 61 EDFVFMKTIORCNTGRSISLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKGDNP 120  
DB 61 EDFVFMKTIORCNTGRSISLNCCEIKSQFEGFYVDIMLNKEETKENSFEMQKGDNP 120  
QY 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKQLTVKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASSKTTSVLQMAEKGYTMSNNLVLTLENGKQLTVKQGLYYIYAQVTFCSN 180  
QY 181 REASSOAPFIASLCLKSGRFRERILLRAANTHSSAKPGQOOSIHJGVFELPGASVFN 240  
DB 181 REASSOAPFIASLCLKSGRFRERILLRAANTHSSAKPGQOOSIHJGVFELPGASVFN 240  
QY 241 VTDPQOVSHGTGFTSFGLKL 261  
DB 241 VTDPQOVSHGTGFTSFGLKL 261

RESULT 11  
US-09-088-913A-12  
Sequence 12, Application US/09088913A  
Patent No. 6087329  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA B.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,913A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-088-913A-12

Query Match 100.0%; Score 1335; DB 3; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSATGIPISMKIFMYLTFLITOMISALPAVYLHRLDKIEDERNH 60  
DB 1 MIETYNQTSPPRSATGIPISMKIFMYLTFLITOMISALPAVYLHRLDKIEDERNH 60  
QY 61 EDFVFMKTIQRCNTERGSLSLNCEIRKSGFEGFYKDIMLNKEETKENSFEMQGDNP 120  
DB 61 EDFVFMKTIQRCNTERGSLSLNCEIRKSGFEGFYKDIMLNKEETKENSFEMQGDNP 120  
QY 121 QIAAHVISEASKTTSTVLQMAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASKTTSTVLQMAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHGAVFELQPGASVFN 240  
DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHGAVFELQPGASVFN 240  
QY 241 VTDPQOVSHGTGFTSFGILKL 261  
DB 241 VTDPQOVSHGTGFTSFGILKL 261

## RESULT 12

US-08-589-771B-8

Sequence 8, Application US/08589771B

Patent No. 6106832

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: DAVISON, BARRY

APPLICANT: FANSLON, WILLIAM

APPLICANT: RENSLOW, BLAIR

APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING

TITLE OF INVENTION: DEFECTIVE CD40L (as amended)

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS-DOS/Windows 95

SOFTWARE: Word for Windows 95, 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/589,771B

FILING DATE: January 22, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY, JANIS C.  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2810-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-589-771B-8

Query Match 100.0%; Score 1335; DB 3; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2e-137;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETYNQTSPPRSATGIPISMKIFMYLTFLITOMISALPAVYLHRLDKIEDERNH 60  
DB 1 MIETYNQTSPPRSATGIPISMKIFMYLTFLITOMISALPAVYLHRLDKIEDERNH 60  
QY 61 EDFVFMKTIQRCNTERGSLSLNCEIRKSGFEGFYKDIMLNKEETKENSFEMQGDNP 120  
DB 61 EDFVFMKTIQRCNTERGSLSLNCEIRKSGFEGFYKDIMLNKEETKENSFEMQGDNP 120  
QY 121 QIAAHVISEASKTTSTVLQMAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
DB 121 QIAAHVISEASKTTSTVLQMAEKGYTMSNNLVLTLENGKQLTVRKQGLYYIYAQVTFCSN 180  
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHGAVFELQPGASVFN 240  
DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPGQOSIHGAVFELQPGASVFN 240  
QY 241 VTDPQOVSHGTGFTSFGILKL 261  
DB 241 VTDPQOVSHGTGFTSFGILKL 261

## RESULT 13

US-08-769-819-12

Sequence 12, Application US/08769819

Patent No. 6264951

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLON, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: Microsoft Word for Apple, version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/769,819

FILING DATE: 19-DEC-1996

```
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-769-819-12

Query Match      100.0%; Score 1335; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 2e-137;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETNOTSPRSATGPIPSMKIFMYLITVFLITOMIGSALPAYLHRLDKIEDERLH 60
DB 1 MIETNOTSPRSATGPIPSMKIFMYLITVFLITOMIGSALPAYLHRLDKIEDERLH 60
QY 61 EDFVFMKTIOCRNTGERSLSLNCEEIKSQPEGFVKDMLNKEETKENSPEMOKGQNP 120
DB 61 EDFVFMKTIOCRNTGERSLSLNCEEIKSQPEGFVKDMLNKEETKENSPEMOKGQNP 120
QY 121 QIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTLENGKOLTVRQGLYYIYAQVTCNS 180
DB 121 QIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTLENGKOLTVRQGLYYIYAQVTCNS 180
QY 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGAVFELQPGASVFN 240
DB 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGAVFELQPGASVFN 240
QY 241 VTDPQVSHGTGFTSFGLKL 261
DB 241 VTDPQVSHGTGFTSFGLKL 261

RESULT 14
US-08-770-974-12
Sequence 12, Application US/08770974
Patent No. 6290972
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
```

```
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,974
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-770-974-12

Query Match      100.0%; Score 1335; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 2e-137;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIETNOTSPRSATGPIPSMKIFMYLITVFLITOMIGSALPAYLHRLDKIEDERLH 60
DB 1 MIETNOTSPRSATGPIPSMKIFMYLITVFLITOMIGSALPAYLHRLDKIEDERLH 60
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QY 121 QIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTLENGKOLTVRQGLYYIYAQVTCNS 180
DB 121 QIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTLENGKOLTVRQGLYYIYAQVTCNS 180
QY 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGAVFELQPGASVFN 240
DB 181 REASSQAPFIASCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGAVFELQPGASVFN 240
QY 241 VTDPQVSHGTGFTSFGLKL 261
DB 241 VTDPQVSHGTGFTSFGLKL 261

RESULT 15
US-08-858-197-4
Sequence 4, Application US/08858197
Patent No. 6297052
GENERAL INFORMATION:
APPLICANT: KERRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
DIFFERENTIATING B CELLS, AND USES THEREOF
```

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;
; NUMBER OF SEQUENCES: 4
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 100 NEW YORK AVE. N.W. SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,580
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-858-197-4
;
Query Match 100.0%; Score 1335; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 2e-137;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCQOQSIHLGVFELQPGASVFN 240
QY 241 VTDPQOVSHGTGFTSFGLKL 261
DB 241 VTDPQOVSHGTGFTSFGLKL 261
;
RESULT 16
; US-08-770-981-12
; Sequence 12, Application US/0870981
; Patent No. 6391637
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION

```

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;
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,981
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-770-981-12
;
Query Match 100.0%; Score 1335; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 2e-137;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
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DB 1 MIETYNQTSPPSAATGPIISMKIEMVLLTVFLITQMIGSALFAVYLHRLDKIEDERNLH 60
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DB 61 EDFVFMKTIOKCNTEGERSLSLNCBEIKSQEPGFYKDIMLNKEETKKESEFMOKGDONP 120
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DB 121 QIAAHVISEASKTTSVLOMAEKGYTMSNNLVLTLENGKQLTVKROGLYYIYAQVTFCSN 180
QY 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCQOQSIHLGVFELQPGASVFN 240
DB 181 REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCQOQSIHLGVFELQPGASVFN 240
QY 241 VTDPQOVSHGTGFTSFGLKL 261
DB 241 VTDPQOVSHGTGFTSFGLKL 261
;
RESULT 17

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US-09-399-106-12  
; Sequence 12, Application US/09399106  
; Patent No. 6410711  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/399,106  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-399-106-12

Query Match  
Best Local Similarity 100.0%; Score 1335; DB 4; Length 261;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MIETYNQTSPPSAATGLPISMKIFMYLITVFLITOMIGSALFAVYLHRLDKIEDERNH 60  
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Qy 121 QIAAHVISEASSKTSVLYQMAEKGYTMSNNLVTLNKGKQLTVRQGLYYIYAQVTFCSN 180

Db 121 QIAAHVISEASSKTSVLYQMAEKGYTMSNNLVTLNKGKQLTVRQGLYYIYAQVTFCSN 180  
Qy 181 REASSQAPFLASLCLKSPGPFERILLRAANTHSSAKPCGQOSIHLGVFELQPAASVFN 240  
Db 181 REASSQAPFLASLCLKSPGPFERILLRAANTHSSAKPCGQOSIHLGVFELQPAASVFN 240  
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241 VTDPSQVSHGTGFTSFGLKL 261

RESULT 18  
PCT-US93-10034-4  
; Sequence 4, Application PC/TUS9310034  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/10034  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 1003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US93-10034-4

Query Match  
Best Local Similarity 100.0%; Score 1335; DB 5; Length 261;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 EDFVFMKTIORCNTERGERSLNLNCEIISQPEGFVKDMLNKEETKENSPEMKGDNP 120  
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181 REASSQAPFLASLCLKSPGPFERILLRAANTHSSAKPCGQOSIHLGVFELQPAASVFN 240  
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241 VTDPSQVSHGTGFTSFGLKL 261

Sat Jun 7 13:51:25 2003

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Page 11

Db 241 VTDBSQVSHGTGFTSFGLKLT 261

Search completed: June 7, 2003, 14:11:52  
Job time : 27 secs